Res

SUMMARIES

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Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q-/cgn2_1/USPTQ_spool/US10008355/runat_17122002_112336_14573/app_query.fasta_1...
-DB=N_Geneseq_101002 -QFMT-fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000
-USER=US1000835_@CGN_1_1_0_@trunat_17122002_11236_14573 -NCPU=6 -ICPU=3
-NC_XLPXY -NC_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPPXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
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                  US-10-008-355-25
54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2185239 seqs, 1125999159 residues
SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
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Listing first 45 summaries
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pr and is derived by analysis of the total score distribution. printed. ۵

ALIGNMENTS

ESULT 1	
D	AAV75063 standard; DNA; 1019 BP. UWW.
×	
a	AAV75063;
×	
H	16-MAR-1999 (first entry)
×	
Ħ	Staphylococcus aureus contig SEQ ID #752.
×	
Σ	Computer readable medium; vaccine; S.aureus infection;
Σ	cellulitis; eyelid infection; food poisoning; osteomyel
Σ	skin infection; surgical wound infection; scalded skin
Σ	toxic shock syndrome; ds.
×	
S	Staphylococcus aureus.
×	
H	Key Location/Qualifiers

TX OX K K K K X D X D X A X H A R immunodetection; litis; therapy; syndrome;

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RESULT 2
AAQ27988
                                                                                                                                                                                                                                                            US-10-008-355-25 (1-10) x AAV75063 (1-1019)
                                                                                                                                                                                                                                                                                                   Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S. aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importeance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S. aureus infection. The polypeptides can also be used in a kit for the immunodetection of S. aureus in a sample. S. aureus is implicated in numerous human diseases, including cellulitis, expelid infections, food poisoning, osteomyelitis, with and surroical wound infections food poisoning, osteomyelitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                     Protease from S. Aureus
                                                      11-FEB-1993
                                                                                        AAQ27988;
                                                                                                                      AAQ27988 standard; DNA; 1558
                                                                                                                                                                                                                                                                                                                                  Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1019 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 1646-1647; 3271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stored on computer readable medium
anti-S.aureus vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide(s) and proteins derived stored on computer readable medium and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-374922/35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JAN-1996;
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                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             901..960
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequences given in AAQ27987-88 encode proteases which were isolated from Staphylococcus aureus strains. The DNA sequences were isolated by PCR using the primer sequences given in AAQ27960-86. The protease specifically cleaves the peptide bond at the C-terminus of the glutamic acid residue in polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel protease prepd. using Bacillus or Saccharomyces host capable of cleaving peptide bond at carboxyl terminus of glacid residues in polypeptide(s)
mat_peptide
                                sig_peptide
                                                                                                                      Staphylococcus
                                                                                                                                                         Protease; PCR;
                                                                                                                                                                                                                           11-FEB-1993
                                                                                                                                                                                                                                                             AAQ27987;
                                                                                                                                                                                                                                                                                                AAQ27987 standard; DNA; 1586
                                                                                                                                                                                                                                                                                                                                                                    1050 ACTGGTGGTAATTCAGGTTCACCTGTATTT 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1558 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                   1 ThrGlyGlyAsnSerGlySerProValPhe 10
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                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                         S. Aureus ATCC12600
                                                                                                                      aureus.
                                                                                                                                                     amplify; Staphylococcus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90JP-0040398
/*tag= a
352..555
/*tag= b
556..1425
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558..1361
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354..557
                                                                352..1425
                                                                                  Location/Qualifiers
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Best Score:

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RESULT 4
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Query Match:
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequences given in AAQ27987-88 encode proteases which were isolated from Staphylococcus aureus strains. The DNA sequences were isolated by PCR using the primer sequences given in AAQ27960-86. The protease specifically cleaves the peptide bond at the C-terminus of the
                                                                                                                                                                                                                                                                                                                                             1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel protease prepd. using Bacillus or Saccharomyces capable of cleaving peptide bond at carboxyl terminus acid residues in polypeptide(s)
                                                                                                                                                                                              Dipeptidylpeptidase-7; DPP-7; gene; ds; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; gingivitis;
                                                                                                                                                                                                                                                      05-SEP-2002
                                                                                                                                                                                                                                                                                                 AAL43635 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1586 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 13-15; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-304938/37.
P-PSDB; AAR26842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP04211370-A
                     08-NOV-2000; 2000US-246827P
                                                                                       WO200238742-A2
                                                                                                                                                                 Porphyromonas
                                                                                                                                                                                                                                Porphyromonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glutamic acid residue in polypeptide.
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(UYGE-) UNIV GEORGIA RES FOUND INC.
                                           08-NOV-2001; 2001WO-US46782
                                                                 16-MAY-2002.
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                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                               gingivalis.
                                                                                                                                                                                                                              gingivalis dipeptidylpeptidase-7 (DPP-7) coding sequence
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                                                                                                       /*tag= a
/product= "Porphyromonas gingivalis DPP-7"
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Indels:
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Matches:
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RESULT 5
AAH52485
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidylepptidase-7 (PPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present DNA sequence encodes the Porphyromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1930 ACGGGCGTAACTCCGGTAGCCCCGTATTC 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated dipeptidylpeptidase useful for identifying inhibitor the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis -
Nucleic acids encoding useful for vaccinating
                                         WPI; 2001-316495/33.
P-PSDB; AAG81635.
                                                                                                                                                                                                                                                           Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                     Staphylococcus epidermidis SR1
                                                                                                                                                                                                                                                                                                                                                              03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                           AAH52485;
                                                                                                                                                                                                                                                                                                                                                                                                                      AAH52485 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2139 BP; 544 A; 543 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Fig 4; 65pp;
                                                                                                                                                                         09-NOV-2000;
                                                                                                                                                                                                     17-MAY-2001.
                                                                                                                                                                                                                                  WO200134809-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Travis J,
                                                                                                                                              09-NOV-1999;
                                                                                                                                                                                                                                                                                         vaccination;
                                                                                                                (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                  epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ThrGlyGlyAsnSerGlySerProValPhe 10
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                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                        endocarditis; ds.
                                                                                                                                                                         2000WO-US30782.
                                                                                                                                                                                                                                                                                                                                  open reading
                                                                                                                                            99US-0164258
                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.73
54.00
100.00%
100.00%
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24
polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                       849
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                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                  frame nucleotide sequence SEQ
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                                                                                                                                                                                                                                                                                                     strain; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   565 G; 487 T; 0 other;
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Conservative:
Mismatches:
Indels:
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RESULT 6
ABN91429
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH52304 to AAH53970 represent nucleic actus (1) encouring polypermi (II), given in AAG81454 to AAG83120, from Staphylococcus epidermi (I) and (II) can have antibacterial activity and therefore can be in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                              14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                             US6380370-BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus
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                                                                                                                                                         Doucette-Stamm
                                                                                                                                                                                                                                                                                                                                        13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                           30-APR-2002
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                                                                               P-PSDB; ABP38884.
                                                                                                                                                                                                         (GENO-) GENOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABN91429 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             694 GGTGGAAACTCTGGATCTCCAGTATTT 720
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                                                                                                       2002-381255/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                       ĽA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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                                                                                                                                                                                                                                                         97US-064964P
                                                                                                                                                                                                                                                                                   97US-055779P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epidermidis ORF nucleic acid sequence SEQ ID NO:892.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene;
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Conservative:
Mismatches:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
           S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
                                                                                                                                           Claim 8;
                                                                                                                                                                       Nucleic acids encoding useful for vaccinating
                                                                                                                                                                                                                         WPI; 2001-316495/33.
                                                                                                                                                                                                                                                                                                                                                                                                                 WO200134809-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S. epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH54330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH54330 standard; DNA; 3189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USPTO web site.
                                                         AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (II) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the
                                                                                                                                                                                                                                                        Kimmerly
                                                                                                                                                                                                                                                                                                                                                   09-NOV-2000; 2000WO-US30782
                                                                                                                                                                                                                                                                                                                                                                                    17-MAY-2001
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                                                                                                                                                                                                                                                                                      (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No.:
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vaccinate subjects and
                                                                                                                                        Page 1307-1308; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                       99US-0164258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genomic polynucleotide sequence SEQ ID NO:3694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 A;
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90.74%
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                                                                                                                                                                       polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis -
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 raise antibodies
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Conservative:
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against the bacteria
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AAL17622
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                                                                                                                                                                                                                                                                                                                                                                      14-JAN-2000; 2000US-0176077.
14-MAR-2000; 2000US-0199167.
24-MAR-2000; 2000US-0192099.
29-MAR-2000; 2000US-0193480.
15-MAY-2000; 2000US-021315.
09-JUN-2000; 2000US-021315.
25-JUL-2000; 2000US-0220534.
                                                                                                                                                                                                                                                                                                                                                                                             14 -MAR-2000;
24 -MAR-2000;
29 -MAR-2000;
15 -MAY-2000;
09 -JUN-2000;
                  The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is affilicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for the polynucleotides and encoded polypeptides are potential markers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human breast cancer expressed polynucleotide 10079.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to
                                                                                                                                                       Claim
                                                                                                                                                                                                                                          WPI; 2001-451856/48.
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  detecting, diagnosing,
                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JAN-2001; 2001WO-US00798
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                                                                                                                                                                                             New peptide useful as a marker for the diagnosis of breast cancer
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                                                                                                                                                  Page 1799; 3695pp; English.
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                                                                                                                                                                                                                                                                                   Wang Y,
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100.008
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monitoring,
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Matches:
Conservative:
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
19-MAY-2000;
19-MAY-2000;
07-JUN-2000;
17-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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30-JUN-2000;
07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity.
                                                                                                                                                                                                                                                                                                                                 02-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                               Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                  Human reproductive system related antigen cDNA SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                        cancer; gene therapy;
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                                                                                 2000US-0214886
2000US-0215135
2000US-0216647
2000US-0216880
2000US-0217487
2000US-0217496
2000US-0217496
2000US-0220963
2000US-0220964
2000US-0224518
2000US-0224518
2000US-0224518
2000US-0225213
2000US-0225214
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2000US-0198123.
2000US-0205515.
2000US-0209467.
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2000US-0180628
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2000US-0189874
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RESULT 10
AAX20213
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10.DEC-2000
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05.DEC-2000
06.DEC-2000
08.DEC-2000
09.DEC-2000
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P-PSDB; AAM94047.
  20-APR-1999
                                                    AAX20213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention.
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                                                                                                      standard; DNA; 758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention provides the protein and coding sequences of uman reproductive system related antigens. These can be ention and treatment of reproductive system disorders, ancer. The present sequence is a coding sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0249208
2000US-0249211
2000US-0249211
2000US-0249212
2000US-0249213
2000US-0249214
2000US-0249216
2000US-0249216
2000US-0249216
2000US-0249216
2000US-0249245
2000US-0249245
2000US-0249245
2000US-0249264
2000US-0249297
2000US-0249297
2000US-0249297
2000US-0250160
2000US-0250160
2000US-0251988
2000US-0251856
2000US-0251856
2000US-0251868
2000US-02518868
(first entry)
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Matches:
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22-AUG-2000
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24-SEP-2000
25-SEP-2000
26-SEP-2000
27-SEP-2000
27-SEP-2000
28-NOV-2000
29-SEP-2000
20-OCT-2000
20-OCT

2000US-0226868 2000US-02277099 2000US-0229343 2000US-0229343 2000US-0229343 2000US-0229509 2000US-0229509 2000US-0229513 2000US-0229513 2000US-0231243 2000US-0231243 2000US-0231241 2000US-0231241 2000US-0231241 2000US-0231299 2000US-0233299 2000US-0233299 2000US-0233299 2000US-0233299 2000US-0233299 2000US-0233961 2000US-0233963 2000US-02346476 2000US-0246476 2000US-02464776 2000US-0246526 2000US-0246526 2000US-0246526 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246528 2000US-0246611 2000US-0246611 2000US-0246611

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RESULT 11
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06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes an antigenic polypeptide fragment isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 212-213; 301pp; English.
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            Enterococcus faecalis
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                                                                                                                                                                                                                                                                                                                                                                                           protein activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-070095/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection; attenuation;
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                                    gene;
                                                Enterococcus;
                                                                                                05-AUG-2002
                                                                                                                       ABN98198
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                                                                                                                                              ABN98198 standard;
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                                                                        faecalis
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                                                                                             (first entry)
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                                                vaccine;
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97US-0044031.
97US-0046655.
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                                              gastrointestinal disease; diagnosis; antibiotic;
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RESULT 12
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Query Match:
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06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of a number of polypeptides from Entercoccus faecalis. The proteins can be used as vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal, particularly E. faecalis. The polynucleotide is also useful for preventing or treating E. faecalis infection. The present sequence is a coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                          detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New genes and polypeptides from Enterococcus faecalis, useful vaccines for preventing, treating or attenuating an infection a member of the Enterococcus genus in an animal, particularly faecalis
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P-PSDB; ABP43442.
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Bailey C,
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                                             (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                        attenuation; antigenic; ss.
  Choi GH,
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                                                                                                                                                                                                                                                                                                                                                                                              faecalis; infection; vaccine;
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97US-0044031.
97US-0046655.
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  Kunsch CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis protein
                                                                                                                                                                                                                                                                                                                                         04-MAY-1998;
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                                                                                   New genes and polypeptides from Enterococcus faecalis, useful vaccines for preventing, treating or attenuating an infection
                                                                                                                                                                   P-PSDB;
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            (KIM) cDNA clone. KIM proteins can be administered therapeutically by expressing KIM encoding polynucleotides, to promote growth and/or survival of damaged tissue (e.g. renal tissue), since the KIM proteins are upregulated in injured or regenerating (especially renal) tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of a number of polypeptides from Enterococcus faecalis. The proteins can be used as vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal, particularly E. faecalis. The polynucleotide is also useful for preventing or treating E. faecalis.
                                                                                                                   Kidney injury-associated molecule, KIM, polypeptides - upregulated in injured or regenerating tissues, useful to promote tissue growtl and regeneration, especially to treat renal conditions
                                                                                                                                                                                                                  Cate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 888 BP;
                                                                 The present sequence represents a kidney injury associated molecule
                                                                                             Claim
                                                                                                                                                                         P-PSDB; AAW86338
                                                                                                                                                                                                                                                                     23-MAY-1997;
23-MAY-1997;
                                                                                                                                                                                                                                                                                                             22-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                 WO9853071-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kidney injury associated molecule; kidney injury related molecule; KIM; tissue growth promotion; regeneration; renal condition; acute renal failure; acute nephritis; tumour; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kidney injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV80633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV80633 standard;
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                                                                                                                                                                                                                                         (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                        26-NOV-1998
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fusion proteins,
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                                                                                         Page 186-188; 213pp; English.
                                                                                                                                                                                                                  Hession
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97US-0047490.
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                                                                                                                                                                                                                  Sanicola-Nadel
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RESULT 15
AAX13198/c
ID AAX13198 standard; DNA; 4951
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06-MAY-1997;
16-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapeutically, e.g. these or the KIM proteins may be included with an acceptable carrier in pharmaceutical compositions, useful for therapy/prophylaxis of conditions associated with disfunction/disregulation of KIM genes or proteins, especially renal diseases or impairments of renal function in humans (e.g. acute renal failure, acute nephritis). The
                                                                                           New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
Claim 1; Page 1248-1251; 2084pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAR-1999
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                                                                                                                                                                                                                     WPI; 1999-045171/04.
                                                                                                                                                                                                                                                                              Barash
                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9850555-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis genome contig SEQ ID NO:261.
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97US-0046655.
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Search completed: December 20, Job time: 197.526 secs
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                                                                                                                                                    US-10-008-355-25 (1-10)
                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                       A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                         Sequence 4951 BP;
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                                                                           695 ACCGGCGGTCAATCTGGTTCACCAATCTAT 666
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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-O_cgn2_1/USPTO_spool/US10008355/runat_17122002_112337_14593/app_query.fasta_1.398
-OB-GenEmbl -OPMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-DB-GenEmbl -OPMT=fastap -1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -TRE_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10008355_@CCN_1 1_1616_@runat_17122002_11237_14593 -NCPU=6 -TCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Listing first 45 summaries
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Copyright (c) 1993 - 2002 Compugen Ltd.
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31: em_htg_inv:*
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35: em_htg_rod:*
36: em_htg_rod:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_hum:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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                                                 ACCESSION
                                                                                      E03836
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                       DNA encoding V8 protease
E03836
E03836.1 GI:2172050
JP 1992211370-A/2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yoshikawa,K., Tsuzuki,H., Fujiwara,T., Nakamura,E., Iwamoto,H., Matsumoto,K., Shin,M., Yoshida,N. and Teraoka,H.
Purification, characterization and gene cloning of a novel glutamic acid-specific endopeptidase from Staphylococcus aureus ATCC 12600 Biochim. Biophys. Acta 1121 (1-2), 221-228 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V8-like protease; glutamic acid specific protease
S. aureus (strain ATCC12600) genomic DNA.
Staphylococcus aureus
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           Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (30-OCT-1990) to DDBJ by:
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/db_xref="taxon:1280"
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919. .1089
/note="(ProAsxAsn) sequence"
251 c 202 g 352 t
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Percent Similarity:
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Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
1 (bases; 1 to 1566)
1 (bases, 1 to 1566)
Nakamura, E., Tamaki, M., Teraoka, H., Matsumoto, K.,
Nakamura, E., Tsuzuki, H., Yoshida, N. and Kakudou,
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FT mat_pep
FT
Patent: JP 1992211370-A 1 03-AUG-1992;

SHIONOGI & CO LTD

OS Staphylococcus aureus

PN JP 1992211370-A/1

PD 03-AUG-1992

PD 03-AUG-1992

PR 19-FEB-1991 JP 1991024633

PR 20-FEB-1990 JP 90P 40398
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DNA encoding V8-like protease.
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                                                                                                      NEW PROTEASE
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19-FEB-1991 JP 1991024633
20-FEB-1990 JP 90P 40398
NAKAMURA ETSUO, TAMAKI MIKIO,
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C12N9/52,C12N15/57,(C12N15/57,C12R1:445);
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JP 1992211370-A/2
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*source: clone=pAM82SIGV8;
Feature is identified by similarity;
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hypothetical: No;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Staphylococcus aureus"
/db_xref="taxon:1280"
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Location/Qualifiers
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Best Local Similarity:
Query Match:
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KOICHI,
PI SHIN MA
PI KAKUDOU
PC CLIN9/5
CC strande
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CC hypothe
CC anti-se
CC *source
CC *source
CC Feature
FH Key
FT CDS
FT CDS
Sig_peptide
FT mat_pep
                                                                                                                                                                             South San Francisco, CA 94080, USA
2 (bases 1 to 1634)
Carmona C. and Gray G. L.
Nucleotide sequence of the serine protease gene of Staphylococcus aureus, strain V8
                                                                                                                                                                                                                                                                                                                                                                                         SASP
                                                                                                                                                                                                                                                                                                             serine protease.
Staphylococcus aureus.
Staphylococcus aureus
                                                                                                                                                        Nucleic Acids Res. 15 (16), 87316953
                                                                                                                                                                                                                                Submitted (16-SEP-1987) Gray G., South San Francisco, CA 94080, U
                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus V8 serine
                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                          Gray,G.
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Key Location/Qualifiers
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C12N9/52,C12N15/57,(C12N15/57,C12R1:445);
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*source: clone=pAM82SIGV8;
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Location/Qualifiers
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/db_xref="taxon:1280"
302 c 219 g 476 t
            /note="preproenzyme (AA
/codon_start=1
/transl_table=11
                                                                                       /strain="V8"
                                                                                                                            Location/Qualifiers
/protein_id="CAA68434.1"
                                                               clone="pV8CO"
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Infect. Immun. 69 (1), 159-169 (2001)
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Staphylococcus aureus serine protease operon, complete sequence.
AF309515
                                                                                                                                                                                                                                                                                                  Submitted (28-SEP-2000) Laboratory Medicine and Pathobiology, University of Toronto, Sunnybrook and WCHSC, 2075 Bayview Ave Toronto, ON M4N 3M5, Canada
                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 3240)
Rice, K.C. and McGavin, M.J.
Direct. Submission
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                                                                                                                                                                                                                                                                                  Location/Qualifiers
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DB:
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AJ293885.2 GI:22218025
Cysteine proteinase; glutamyl endopeptidase;
proD gene; proM gene; spwl gene.
                                                                                 and msrwl gene.
                                                                                                         Staphylococcus warneri
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cytoplasmic location"
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TITLE
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Submitted (30-AUG-2000) Kakikawa M., Molecular Biology Group,
Toyama University, 3190 Gofuku, Toyama, 930-8555, JAPAN
revised by author (08-AUG-2002)
On Aug 13, 2002 this sequence version replaced gi:9968802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YOKO1,K., Kakikawa,M., Kimoto,H., Watanabe,K., Yasukawa,H., Yamakawa,A., Taketo,A. and Kodaira,K.I. Genetic and biochemical characterization of glutamyl endopeptidase of Staphylococcus warneri M Gene 281 (1-2), 115-122 (2001)
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                                                                            FEATURES
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                                                                                                                                                                     TITLE
JOURNAL
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                                                                                    Direct Submission
Submitted (06-MAR-2002) Akio Oguchi, National Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:oguchi@nite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-8423, Fax:81-3-3481-8424)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus subsp. aureus MW2 (strain:MW2) DNA Staphylococcus aureus subsp. aureus MW2 Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus subsp. aureus strain MW2, section 4/10. AP004825 BA000033 AP004825.1 GI:21203989
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                                                                                                                                                                                                   2 (bases 1 to 290150)
Aoki,K., Oguchi,A., Nagai,Y., Asano,K.,
Kuroda,M., Hiramatsu,K. and Kikuchi,H.
                                                                                                                                                                                                                                                                                                    community-acquired MRSA
Lancet 359 (9320), 1819-1827 (2002)
                                                                                                                                                                                                                                                                                                                                         Genome and virulence determinants of high virulence
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ANQDNOVOYENTLKNEKIREOOFDNSWCAGFSMAALLNATKNTDKYNAHDIMRTLYPN
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IRYEKF"
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                                                                          Location/Qualifiers
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MMYVIGLIVTLGIGSSFATIPIIASLFIPFGASIGLDTMALIALIGTASALGDSGSPA
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complement(7786. .9282)
complement(7786. .9282)
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complement(6678..7034)
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                               complement (9275.
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FYGKFFIVQSTFERGFYLSGVIVLLSSLVVLYSVIRIFLQGFFGQPKGYDLNNKVDVK
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LPGRFYVITLYRIIKLVIIFLIELIKANFDVLKIIIKPSIKNEPGFFVYHTDLKKDWQ
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Best Local Similarity:
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Technology and Evaluation, Biotechnology Center; 2Chome 49. Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:oguchi@nite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-8424, Fax:81-3-3481-8424) On Jun 12, 2001 this sequence version replaced gi:13700734. Location/Qualifiers
                                                                                                                                                          Aoki,K., Oguchi,A., Hosoyama,A., Nagai,Y., Kuroda,M., Hiramatsu,K. and Kikuchi,H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                 Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I., Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M., Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A., Mizutani-Ui,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C., Sekimizu,K., Hirakawa,H., Kuhara,S., Goto,S., Yabuzaki,J., Kanehisa,M., Yamashita,A., Oshima,K., Furuya,K., Yoshino,C., Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K. Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus subsp. aureus N315 (sub_spestrain:N315) DNA.
Staphylococcus aureus subsp. aureus N315
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome, section 4/10.
AP003132 BA000018
AP003132.2 GI:14349174
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                                                                                                              Submitted (30-JAN-2001) Akio Oguchi, National Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10
                                                                                                                                                                                                                                                                                                                    aureus
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/protein_id="BAB94698.1"
/db_xref="GI:21204000"
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VESMKGVPEDD"
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IPLFILEPVHMTTAVFFDFGVLCAVVGTVMTIIISIGENE"
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/protein_id="BAB94697.1"
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LVQFTEMMLELNKSGNKQQMLNQAPFSFDLSVMAIYPCLASGGTLNLVDKNMINKPKL
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FBSATIVNTYGPTBATVAVTSIQITOEILDQYFTLPGVGVERLGARLSTTDDGELVIEG
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3134 .3370
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WKLIQFISFFTISSGFIDRYKRFVKDDKKVPTGNEYRELVLKAIHMIMLGFLYKYIV
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1902. .3116
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280. .432
/note="(glycerophosphate chain) ORFID:SA0796"
                                                                             /gene="dltD"
3367. .4542
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448. .1905
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3134. .3370
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JOURNAL
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AP003361/c
LOCUS
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AUTHORS
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KEYWORDS
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Best Local Similarity:
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                                                                                                                     Direct Submission
Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College of Medical Technology and Nursing, Department of Medical Technology 1-1-1 Ten-noodai, Tsukuba, Ibaraki 305-8577, Japan (E-mail:tohta@sakura.cc.tsukuba.ac.jp, Tel:81-298-53-3454, Fax:81-298-53-3454)
On May 29, 2001 this sequence version replaced gi:13875305.
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sequence, section 4/9.
APO03361 BA000017
APO03361.2 GI:1424676
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                                                                          Location/Qualifiers
1. .347235
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Mismatches:
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1997. .2959
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1024. .2004
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35. .1021
                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SAV0995"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="oppB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homologue"
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                                                                                                                                                                                                                                                                                                                                                             codon_start=1
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KSAVTDSDGIIKFDRDNKPGITNLISIYAGLTDMPIKDIEAKYEGEGYGKFKGDLAEI
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6783. .7769
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NPITTEFEDLLYMVDGTYYYAVHFDSHVDQEVINDSYSQLLEFAYPTDRTEVYLNDYA
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5943. .6662
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7817. .9625
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5177. .5572
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LERFRATLFRQTMFAEFEHKIHAIEEAGEPLTPTRMNEEYAKLNKLYFGDSVETDED:
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59.1"
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AUTHORS
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                           Submitted (19-JAN-2001) Dubin G., Institute of Molecular Biology, Jagiellonian University, ul. Mickiewicza 3, Krakow 31-120, POLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dubin, G., Chmiel, D., Mak, P., Rakwalska, M., Rzychon, M. and Dubin, Molecular cloning and biochemical characterisation of proteases from Staphylococcus epidermidis
Biol. Chem. 382 (11), 1575-1582 (2001)
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OKIEKLKYPDGDFWKSKMPKIKSK"
complement(10575...10901)
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/gene="yjbM"
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/strain="6746"
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ACCESSION
VERSION
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AX141641
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Staphylococcus epidermidis. Staphylococcus epidermidis
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AF269652.1
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                                                          sequence.
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1 (bases 1 to 849)
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/db_xref="taxon:32630"
/note="synthetic nucleic acid sequence"
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/product="extracellular serine
/product="extracellular serine
/evidence=experimental
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88 c 122 g 204 t
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NEHNQHIGQVVKPATISSNTDTRINENITVTGYPGDKPLATMWESVGKVVYIGGEELR
YDLSTYGGNSGSPVENGKNQVIGIHYGGVDNKYNSSVYINDFVQQFLRNNIPDINIQ"
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2 (bases 1 to 3189)
2 Taylor, J. David., Kimmerly, W.J., Nelsen, A.J., Godlevski, M.M., Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I., Listenbee, S., Ashanti, C., Altshuller, G., Mamo, L., Shepherd, N.S., Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and Fucho, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3189 bp | Sequence 3694 from Patent WO0134809 AXI44972
                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis nucleic acids Patent: WO 0134809-A 3694 17-MAY-2001; GLAXO GROUP LIMITED (GB)
                                                                                                                                                                                                                                                                                                                                                                           synthetic construct.
synthetic construct
artificial sequences.
1 (bases 1 to 3189)
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Drive, Research Triangle Park, North Carolina 27709-3398, USA
Location/Qualifiers
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1 (bases 1 to 318))
Kimmerly, W.J., Taylor, J. David., Nelsen, A.J., Godlevski, M.M.,
Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I.,
Listenbee, S., Ashanti, C., Altshuller, G., Mamo, L., Shepherd, N.S.,
Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
Furdon, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (22-MAY-2000) Departments of Genomic Sciences and Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc.,
                                                                                                                                                                                                                                                                                                                                                             Kimmerly, W.J.
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/strain="SRI"
/db_xref="taxon:1282"
/clone="step.1015e12"
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/db_xref="taxon:32630"
/note="synthetic nucleic acid sequence"
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gene
                                                                                                                                                                                                                                                                                     Docena,C., El-Dorry,H., Facincani,A.P., Ferreira,A.J.S.,
Ferreira,V.C.A., Ferro,J.A., Fraga,J.S., Franca,S.C., Kitajina,J.P., Krieger,J.E., Kuramae,E.E., Laigret,F., Lambais,S.M.R., Leite,L.C.C., Lemos,E.G.M., Lemos,M.C.F., Lemos,E.G.M., Lemos,M.D., F., Lemos,E.G.M., Madeira,A.M.B.N., Mardins,E.A., Machado,J.A., Machado,M.A., Mardira,A.M.B.N., Madeira,A.M.B.N., Mardins,E.A., F., Marino,C.L., Marques,M.V., Martins,E.A.L., Magai,M.A., Miracca,E.C., Miyaki,C.Y., Monteiro,Vitorello,C.B., Moon,D.H., Nagai,M.A., Nascimento,A.L.T.O., Netto,L.E.S., Nhani Jr.A., Nobrega,F.G., Nunes,L.R., Oliveira,M.A., de Oliveira,M.C., de Oliveira,R.C., Pereira,Jr., Fereira,Jr., Fereira,Jr., Roberto,P.G., Rodrigues,V., Jewson, J. J., Denson, J. J., Gensa,Jr., V.E., de Sa,R.G., Santelli,R.V., Jr., M.A., de Sulva,A.P., Terenzi,M.F., Truffi,D., Tsai,S.M., Verjovski-Almeida,S., Vettore,A.L., Zago,M.A., Zatz,M., Meidanis,J. and Setubal,J.C.
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Simpson, A.J.G., Reinach, F.C., Arruda, P., Abreu, F.A., Acencio, M., Simpson, A.J.G., Reinach, F.C., Araya, J.E., Bala, G.S., Baptista, C.S., Balarenga, R., Alves, L.M.C., Araya, J.E., Bove, J.M., Briones, M.R.S., Bueno, M.R.P., Camargo, A.A., Camargo, L.E.A., Carraro, D.M., Bueno, M.R.P., Camargo, A.A., Camargo, L.E.A., Carraro, D.M., Bueno, M.R.P., Camargo, A.A., Camargo, L.E.A., Carraro, D.M., Bueno, M.R.P., Camargo, A.A., Camargo, L.E.A., Casta, M.C.R.,
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                                                                                                                                                                                                          Submitted (02-JUN-2000) Organization for Nucleotide Sequencing Analysis, Bioinformatics Lab - IC/Unicamp, C.P. 6176, Campinas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The genome sequence of the plant pathogen Xylella 
Xylella fasticiosa Consortium of the Organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xylella fastidiosa 9a5c.
Xylella fastidiosa 9a5c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE004008.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing and Analysis
Nature 406 (6792), 151-157 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0910347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 10689)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marino, C.L.
                                                                                                                                                                                                                                                                         Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AE003849
                                                     /organism="Xylella fastidiosa 9a5c"
/db_xref="taxon:160492"
                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:9106961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fastidiosa. The for Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCT 15-JUN-2001
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1351..1662
                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1839.
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/gene="XF1875"
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/gene="xr1872"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="XF1872"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity; putative;
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/gene="XF1871"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1351. .1662
/gene="XF1874"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLIQRQQKRKASP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVLRHVLTQRQQKRKASP"
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/db_xref="GI:9106962"
                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="XF1875"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="XF1873"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transl_table=11
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAF8467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XF1873"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       .2918)
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HQREKAEEEVWKFPKDRYALYASSTLHTVSHKFRIPKKVWSALSVCVTCSVIGLVFWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to GI|479340 (percent identity: 36 %/que alignment coverage: 87.8 %/subject alignment coverage: 90.2 %); identified by sequence similarity; putative; Clocated using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                    /note="similar to SPIP03626 (percent identity: 36 %/query
alignment coverage: 88.0 %/subject alignment coverage:
105.0 %); identified by sequence similarity; putative; ORF
located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"hypothetical protein; identified
similarity; putative; ORF located using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mSKNKIPNQILTGNWAGFQFINGKLVTPERRTIEEWQLRWLSLT
CTLAREWQKMMEEARATAPQGGLAASDPQRITDALQKTVSHKRRHAANETASIIQLRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="hypothetical protein; identified by sequence
similarity; putative; ORF located using Glimmer/RBSfinder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MMEEARATAPQGGLAASDPQRITDAPKKTGLRKRKYPTTGSASI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein"
79.1"
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Glimmer/RBSfinder"
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Glimmer/RBSfinder
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US-10-008-355-25 (1-10)
                                                                                                                             Best Local Similarity:
Query Match:
                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                               . No. :
                                                                                                                                                                                                                                                                                                                                                                                                                    gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="hypothetical protein; identified by sequence
similarity; putative; ORF located using Glimmer/RBSfinder"
/codon_start=1
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SSVIBDGVSTSATFEARSTALVNGVRYYTVPVDISASTLGSLAKVAVRRGMAFYNVYS
MLSGLINGAGWVIDELTHEVMSGPALKEIPVGTVAWWQDRPGDGHVFYSVTPQGLIAP
INAYQSSLSPPQPLVTSSGPSSVSSEWLYHLEGGGEYIGHLSKTDQSVDTSSGLPP
SVILDTDLGQLVRSDPSTVNAVLTDSQTGAVLLTPEIVSALNKLRRSLEDELKASHAP
DQQPSSGGASSPPSSSGTAWPSFCSWASVVCDFIDWVKSDEFLKKPLVPPDVPYYDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to SP|P03625 (percent identity: 36 %/query alignment coverage: 85.1 %/subject alignment coverage: 86.0 %); dentified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MKSYIDRGIAFFSLLSTSSLVFAADAAGASFDAGAAVTALGAIS
GAVALIGAAKLAPAAISVGWKWLKGAIFG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="hypothetical protein; identified by sequence
similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(4481. .4702)
/gene="XF1878"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(4481. .4702)
/gene="XF1878"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PQAKTWSSGLGEGACESPTTIFIEFSGYKTSVEISYQFFCDFAALMRPVVIVIATILA
AYIAGGFRGVKNV"
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similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(2918. .3202)
/gene="XF1876"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSDRSCRCFNTDGYQIDMSVVECRRLLASPLPFNVYHAYVTSSSSAAAVSSSPSSSPS
SSSVSLSSSVSSAPILGSSSVPSSH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MAQQLMSLYCTQYDVEARTCSQQAWMVPPSLLPPISYEDVRILL PHIVMCELVAMGEHELETVVPD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(4724. .4924)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(3195. .4412)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(2918. .3202)
                                                                                                                                                                                                                                                                                                                                                                                                                complement(4931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="XF1879"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (4724. .4924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein"
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/db_xref="GI:9106968"
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/db_xref="GI:9106967"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campoplano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (15-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 66762)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-10F17
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                           sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This record contains 82 individual
                                                                                                                                                                  be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seg.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu ------ Project Information Center project name: L23222 Center clone name: 10_F_17
    818 1529:
1530 1629: gap
1 717: contig of 717 bp in length
718 817: gap of 100 bp
818 1529: contig of 712 bp in length
1530 1629: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66762 bp
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16 5705

10 642: contig of ...

23 6522: gap of 100 bp

13 7192: contig of 670 bp in le

19 7292: gap of 100 bp

29 8001: contig of 709 bp in l

3002 8101: gap of 100 bp

8807 8906: gap of 100 bp

8907 9620: contig of 705 bp in l

9621 9720: gap of 100 bp

9721 10406: contig of 714 bp in

10507 11232: contig of 686 bp in

10407 10506: gap of 100 bp

11233 11332: gap of 100 bp

11233 11332: gap of 100 bp

12056 12155: gap of 100 bp

12056 12155: contig of 726 bp in

12056 12155: gap of 100 bp

12156 12887: contig of 732 bp

12056 12157: qap of 100 bp

length length length length length

length

100 bp 0422: contig of 717 bp 23 6522: gap of 100 hn 13 7192: con+4

bp in length

2339: contig of 2439: gap of 2439: gap of 2346: gap of 2365: contig of 4065: gap of 244 4893: gap of 244 4893: gap of 244 4893: gap of 245 4893: gap of 246 5705: gap of 246 5705: gap of 246 5705: gap of 247 5705: gap of 248 570

793: contig of 728 bp in gap of 100 km

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13717 13816: gap of 100 bp 13817 14539: contig of 723 bp 14540 14639: gap of 100 bp 14640 15344: contig of 705 bp 15345 15444: gap of 100 bp 15445 16157: contig of 713 bp

12987: gap of 1 13716: contig of

bp in length

16257: gap of 100 b 16968: contig of 711 17068: gap of 100 b 17781: contig of 713

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17881: gap of 100 bp 18602: contig of 721 bp

Qy 1 ThrGlyGlyAsnSe	US-10-008-355-25 (1-1	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity Query Match: DB:	31748 32460 3250 33278 34087 341	· * 3164
snSerGlySerProValPhe 10	lO) x AC121125 (1-66762)	7.34e+03 Length: 45.00 Matches 90.00% Conserv 80.00% Mismatc 83.33% Indels: 2 Gaps:	3259; contig of 71 3259; gap of 10 3259; gap of 10 3377; gap of 34086; contig of 70 34186; gap of 34092; contig of 70 34181; gap of 35814; gap of 35814; gap of 36543; contig of 72 3643; contig of 72 3643; gap of 38191; contig of 72 38291; gap of 39012; contig of 72 38291; gap of 40739; gap of 41453; contig of 72 41453; gap of 41453; gap of 41453; contig of 72 42275; gap of 441453; contig of 72 42375; gap of 441453; contig of 72 44275; gap of 44275; gap of 44275; gap of 443905; contig of 72 44593; contig of 72 44688; gap of 47136; contig of 72 44689; gap of 47136; contig of 72 46416; gap of 47136; contig of 72 47136; gap of 47136; contig of 72 47136; contig of 72 47136; gap of 5713; gap of 5717; contig of 72 5713; gap of 5717; contig of 72 5713; gap of 5717; contig of 73	31747: gap of 100
		66762 :: 8 ative: 1 :hes: 1	2 bp in length bp bp bp in length	

18603 18702: gap of 100 bp 119500 20331: contig of 732 bp in 19400 19499: gap of 100 bp 119500 20331: contig of 732 bp in 20332 20331: gap of 100 bp 20332 2136: gap of 100 bp 2137 2136: gap of 100 bp 2137 2136: gap of 100 bp 21363 2701: contig of 736 bp in 2163 21963 22701: contig of 739 bp in 2163 22701: contig of 739 bp in 22702 2801: gap of 100 bp 23514 23613: gap of 100 bp 23514 23613: gap of 100 bp in 23514 23613: gap of 100 bp in 24427 25244: gap of 100 bp 2545 25244: gap of 100 bp in 25961 26060: gap of 100 bp in 26078: contig of 718 bp in 26078: contig of 718 bp in 26078: contig of 718 bp in 26079 26878: gap of 100 bp 27575 27674: contig of 722 bp in 28397 28496: gap of 100 bp 29174 29273: gap of 100 bp 29174 29273: gap of 100 bp 30025: contig of 722 bp in 30826 30925: gap of 100 bp 30826 30925: gap of 100 bp in 30826 30926 30925: gap of 100 bp in 30826 30926 30926 30926 30926 30926 30

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US-08-626-169-2

US-09-164-907-2

US-07-723-002C-5

US-07-624-313-3
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7.0
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          Sequence 726, App
Sequence 892, App
Sequence 1045, App
Sequence 427, App
Sequence 425, App
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 123, App
                                                                                                                                                                       Description
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US-09-221-017B-726
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 726, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP29:
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
                                                                                                                                         FILING DATE: 23-DEC-
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/221,017B
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOER:
STREET: 755 PAGE MILL ROAD
                                                                                       APPLICATION NUMBER: PP11
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP15
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM.TYPE: Diskett
                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Win
                                                                                                                                                                                                                                                                                                                  STREET: 755 PAGE CITY: Palo Alto
                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94304-1018
APPLICATION NUMBER: FILING DATE: 10-DE
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                                                                                                                                                                                                                                                   Diskette
JMBER: PCT/AU98/01023
10-DEC-1998
                                                                            30-JAN-1998
                                                                                                                                                                       23-DEC-1998
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                                                                                          PP1546
                                                                                                                                 PP1182
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US-99-061-709-6
US-08-225-224-31
US-08-225-224-31
PCT-US95-04468-31
US-08-255-224-31
US-08-680-22
US-08-680-21
US-09-499-884-11
US-09-499-884-11
US-09-221-0178-38
US-08-680-326-13
US-09-221-0178-38
US-09-221-0178-38
US-09-221-0178-38
US-09-221-0178-38
US-09-221-0178-38
US-09-221-0178-38
US-08-64-121-1
US-08-914-848-3-21
US-08-914-848-3-21
US-08-064-121-1
US-08-063-016-23
US-09-063-016-23
US-08-063-016-23
US-08-063-016-23
US-08-063-01459-1
US-08-673-768-1
US-08-673-768-1
US-08-673-768-1
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8, Appli 31, Appli 31, Appli 31, Appli 28, Appli 28, Appli 21, Appli 31, App

Sequence Sequence Sequence Sequence

Sequence

ATTORNEY/AGENT INFORMATION:

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                                                                                                                                                                                                                   SEQ ID NO 892
LENGTH: 936
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-892
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                                                            US-10-008-355-25 (1-10) x US-09-134-001C-892 (1-936)
                                                                                                           Query Match:
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Best Local Similarity:
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                                                                                                                         Best Local Similarity:
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                                                                                                                                          Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 892, Application US/09134001C
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1524 ACGGGCGGTAACTCCGGTAGCCCCGTATTC 1553
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LENGTH: 1974 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 650-813-5600
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                                                                                                                                                                         NO . .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ThrGlyGlyAsnSerGlySerProValPhe 10
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RESULT 3
US-09-221-017B-1045
                                                     US-10-008-355-25 (1-10) x US-09-221-0178-1045 (1-2384)
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Query Match:
                                                                                                                                                              Score:
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                                                                                                                                        Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION UMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/AU98
PRIOR APPLICATION DATA:
10-DEC-1998
APPLICATION UMBER: PCT/AU98
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
ADME: GLAZE: U
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: TELEFAX: 706141
                                                                                                                                                                                                                                                                                                       ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 650-494-0792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304-1018
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                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2384 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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1 ThrGlyGlyAsnSerGlySerProVal 9
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                                                                                                     100.00%
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                                                                                                     Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              score:
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                                                                                                                 Sequence 425, Application US/09071035
Patent NO. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PB36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 427:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6448043
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APPLICANT: G11 H. Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MSDO:
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                             575 ACCGCCGCTCAATCTGGTTCACCAATCTAT 604
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                STATE: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                   CITY: Rockville
                                                                  STREET:
                                                                                ADDRESSEE:
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                                                                                  Human Genome Sciences, Inc
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-008-355-25 (1-10) x US-09-071-035-425 (1-888)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08035634 Patent No. 5459064 GENERAL INFORMATION:
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            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/782,372
FILING DATE: 24-0CT-1991
APPLICATION NUMBER: Japanese Patent
APPLICATION NUMBER: Application No.
FILING DATE: October 24, 1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EPSON PC-286 Book type laptop
OPERATING SYSTEM: MS-DOS 2.11
SOFTWARE: Wordstar 5.0
CURRENT APPLICATION DATA:
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STREET: DAL
STREET: Menlo Park
CTATE: California
GTATE: GTATE
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TITLE OF INVENTION: A No. 5459064el Protease
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS: .
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NAME: A. Anders Brookes
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OPERATING SYSTEM:
SOFTWARE: ASCII
                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                    ZIP: 94025
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BOZICEVIC, KARL
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Matches:
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                                                   5459064 2-288110
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TELEPHONE: (415) 677-7000

REGISTRATION NUMBER:

28,807

29900-20298.00

REFERENCE/DOCKET NUMBER:

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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 856, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Philip
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                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1094 GGAGGACAAAGCGGTTCACCGGTATTC 1120
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LENGTH: 1448 base pair:
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CITY: Research Triangle Park
STATE: No. 6239264th Carolina
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LOCATION: 323 to 1270
IDENTIFICATION METHOD: by experiment
NAME/KEY: signal peptide
LOCATION: 323 to 604
IDENTIFICATION METHOD: by experiment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: mature peptide LOCATION: 605 to 1270 IDENTIFICATION METHOD: b
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                                                                                                                                                      COUNTRY:
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   APPLICATION NUMBER:
                                                                                                                                                                                                                                  ADDRESSEE:
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Steiner, Sabine
Mohr, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                              Philippsen, Peter
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88.89%
88.89%
79.63%
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US/08/998,416
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Matches:
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Best Local Similarity:
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TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Russell, D
APPLICANT: Thigpen, A
TITLE OF INVENTION: B
TITLE OF INVENTION: A
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . No.:
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MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 743 base pairs
TYPE: nucleic acid
                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Corder, Timothy S.
                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587
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                                                                                                                                                                                                                                                                                             COUNTRY: Un:
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                                                                                                                                      APPLICATION NUMBER: FILING DATE: Concur CLASSIFICATION: 435
                                                                    NAME: Corder, Timothy S. REGISTRATION NUMBER: 38, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: CH 0016/97 FILING DATE: 31-DEC-1996
                                                                                                                                                                                                                                                                                                                                      STATE:
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                                                                                                                                                                                                                                                                                                                                                     Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08626169
                                                                                                                                                                                                                                                                                                                                     Texas
                                                                                                                                                                                                                                                                                                                                                                     P.O. Box 4433
                                                                                                                                                                                                                                                                                                                   United States
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74.07%
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Anice E.
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                                                                                      38,414
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Matches:
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Best Local Similarity:
Query Match:
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US-09-164-907-2
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA; Homo sapiens US-09-164-907-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: RUSSELL, DAVID W.
APPLICANT: THIGPEN, ANICE E.
APPLICANT: THIGPEN, ANICE E.
TITLE OF INVENTION: BIOMARKERS FOR DETECTION, DIAGNOSIS AND PROGNOSIS OF
TITLE OF INVENTION: PROSTATE CANCER
FILE REFERENCE: URCO: 021
CURRENT APPLICATION NUMBER: US/09/164,907A
CURRENT FILING DATE: 1998-10-01
EARLIER APPLICATION NUMBER: 08/626,169
EARLIER FILING DATE: 196-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 240
                                                                                                                                                                                 Sequence 5, Application US/07723002C Patent No. 5447862 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09164907A Patent No. 6090559
                                                        APPLICANT: Kester, Hermanus Cornelis Maria
TITLE OF INVENTION: No. 5447862el Expression System
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                        APPLICANT:
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                                                                                                                                                                    APPLICANT:
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STRANDEDNESS: single
TOPOLOGY: linear
                     ADDRESSEE: CIBA-GELGE CONTREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                              2 GlyGlyAsnSerGlySerProValPhe 10
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              Hawthorne
New York
                                                                                                                     Meyhack, Bernd
Gysler, Christof
Visser, Jacob
                                                                                                                                                                    Heim, Jutta
                                        CIBA-GEIGY Corporation
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77.78%
77.78%
72.22%
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Matches:
Conservative:
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Matches:
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Indels:
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TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY:
LOCATION:
LOCATION:
                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /transl_except= (pos: 1541 .. 1543, aa: Tyr) FEATURE:
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IMMEDIATE SOURCE:
CLONE: Plasmid pGW830 (DSM 4389)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 29-JAN-PRIOR APPLICATION DATA:
                                                            LOCATION:
FEATURE:
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                                                                                                                                                                                    FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 24-JUL-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-JUN-: PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
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NAME/KEY:
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REGISTRATION NUMBER: 33,071
REFERENCE/DOCKET NUMBER: 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: GB 8818046.8 FILING DATE: 28-JUL-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: GB 8 FILING DATE: 04-FEB-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
NAME/KEY:
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nucleic acid
NDEDNESS: double
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exon
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1338..1399
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..2112, 2170..2502)
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1194..1337
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1400..1542
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1134..1193
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26-JUN-1989
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Alignment Scores: Pred. No.:
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Best Local Similarity:
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CURRENT FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 174
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 123
LENGTH: 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yuqiu, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun for the Treatment and Diagnosis of Breast Cancer
TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 210121.470
                                                                  NAME/KEY: modified_base LOCATION: (502)
OTHER INFORMATION: Where n
                                                                                                                                                                                                                       LOCATION: (373)
OTHER INFORMATION: Where n
NAME/KEY: modified_base
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LOCATION: (152)
OTHER INFORMATION: Where n
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OTHER INFORMATION: Where n
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OTHER INFORMATION: Where n
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Best Local Similarity:
Query Match:
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US-07-624-313-3/c
                             Best Local Similarity:
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              Query Match:
                                           Percent Similarity:
                                                            Score:
                                                                          Pred.
                                                                                       Alignment Scores:
                                                                                                                      US-07-624-313-3
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 8904100-8
FILING DATE: 05-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Ryan, John W.
REGISTRATION NUMBER: 33,771
REFERENCE/DOCKET NUMBER: 1103326-8:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
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APPLICANT: E
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
                                                                                                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 663 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: both
                                                                                                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL:
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                                                                          No . :
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TELEPHONE: 212-354-8113
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                                                                                                                                      CLONE:
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            Conservative: Mismatches: Indels:
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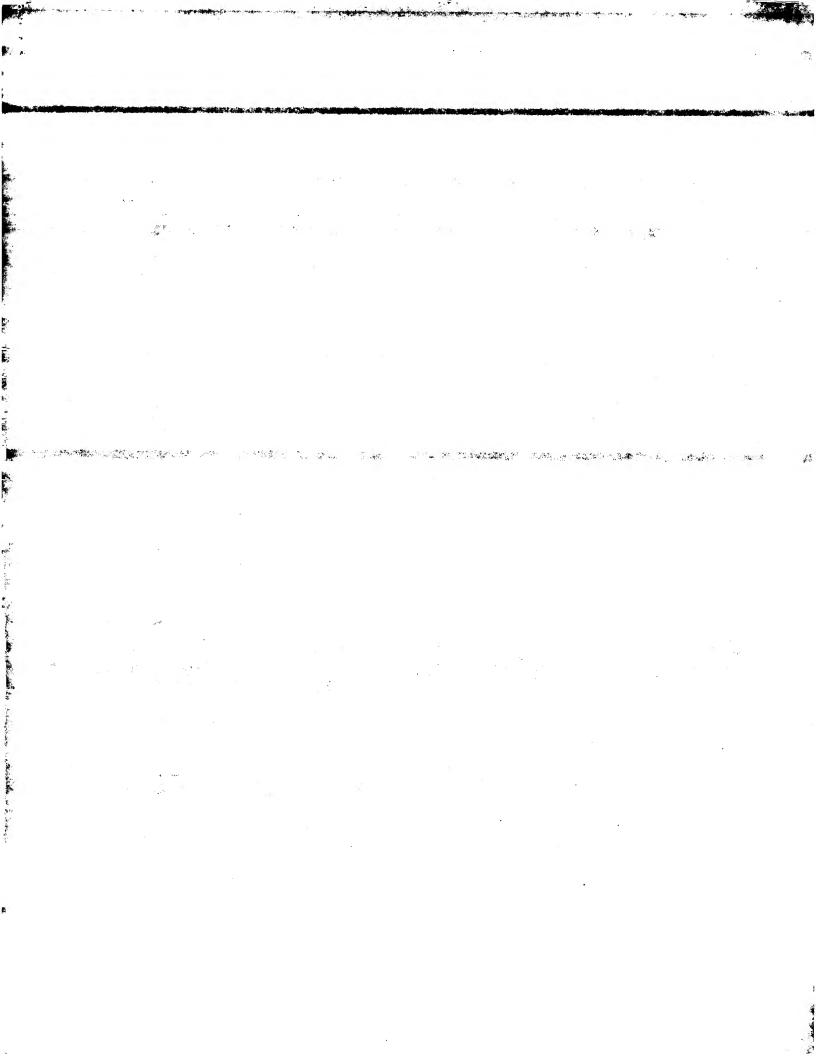
Gaps:

US-10-008-355-25 (1-10) x US-07-624-313-3 (1-663)

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Pred. No.:
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Best Local Similarity:
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                                         Alignment Scores:
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                                                                                                                                                                  SEQ ID NO 6
LENGTH: 3412
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APPLICANT: Stockert, Elisabeth
APPLICANT: Jager, Elke
APPLICANT: Jager, Elke
APPLICANT: Muth, Alexander
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
FILE REFERENCE: LUD 5538
CURRENT APPLICATION NUMBER: US/09/061,709B
CURRENT FILING DATE: 1998-04-17
                                                                                                                                                                                                                                                                       APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
APPLICANT: Gran, Solam
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Jager, Elke
APPLICANT: Knuth, Alexander
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
FILE REFERENCE: LUD 5538
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APPLICANT: Gure, Ali
                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/061,709B CURRENT FILING DATE: 1998-04-17
                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3283
TYPE: DNA
                                                                                                                                              TYPE: DNA
                                                                                                                      ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 GGAGGAAACAGTGGGAAACCTGGATTT 194
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38.00
90.00%
70.00%
70.37%
962
38.00
Length:
Matches:
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QΥ
                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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US-08-225-224-31/c
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В
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                                                                    US-10-008-355-25 (1-10) x US-08-225-224-31 (1-39)
                                                                                                                                                                                                                                                     , MOLECULE TYPE: US-08-225-224-31
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                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 31, Application US/08225224 Patent No. 5635599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,224
FILING DATE: 8-APR-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 543-50/
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Steurisco
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PASTAN, Ira
APPLICANT: KREITMAN, KOBERT J.
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTED FUSION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2535 ACTCACGCAGTTCTGGATCACCTGTGTAT 2564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 94105-1493
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                      1 ThrGlyGlyAsnSerGlySerPro
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                                                                                                                                                                                                Length:
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Search completed: December 20, 2002, 14:11:50 Job time: 42.4211 secs



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-MODEL-frame+p2n.model -Dev=x1h
-Q-ycgn2_1/USPTO_spool/US10008355/runat_17122002_112339_14635/app_query.fasta_1.398
-DB-Published_Applications_NA -QFMT-fastap -SUFFIX-p2n.rnpb -MINMATCH-0.1
-LOOPEL-0 -LOOPEXT-0 -UNITS-bits -START=1 -END=-1 -MATRIX-blosum62
-TRANNS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN-0 -ALIGN=15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXLEN-2000000000 -USER-US10008355_@CGN_1_1_21 @runat_17122002_112339_14635
-NCPU-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP=6
-FGAPEXT-7 -YGAPOP=10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
                                                                                                                      Result
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Maximum DB
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Perfect score:
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length: 2000000000
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Ygapop 10.0 , y
Fgapop 6.0 , I
Delop 6.0 , I
    100:0
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Match Length DB
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Listing first 45 summaries
                                                                                                                                                                                                                                                                          : /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
    /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
    /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
    /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
    /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
    /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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0 US-09-070-927A-261
0 US-09-974-300-327
0 US-09-867-701-1705
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99.214 Million cell updates/sec
Sequence 1, Appli
Sequence 261, App
Sequence 327, App
Sequence 1705, Ap
                                                                                                Description
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                                                         Score:
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                                                                                                                                                                                            SEQ ID NO 1
LENGTH: 2139
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\$\text{S:09-770-444-5}\$\text{S:09-770-444-5}\$\text{S:09-783-590-6}\$\text{S:09-783-590-6}\$\text{S:09-783-590-6}\$\text{S:09-783-590-6}\$\text{S:09-783-590-6}\$\text{S:09-808-701-1}\$\text{S:09-808-701-1}\$\text{S:09-809-651-8}\$\text{S:09-804-761-1}\$\text{S:09-804-761-1}\$\text{S:09-804-761-1}\$\text{S:09-815-242-6}\$\text{S:09-815-242-6}\$\text{S:09-815-242-6}\$\text{S:09-815-242-6}\$\text{S:09-815-242-6}\$\text{S:09-804-761-1}\$\text{S:09-804-761-1}\$\text{S:09-804-761-1}\$\text{S:09-804-761-1}\$\text{S:09-804-761-1}\$\text{S:09-804-761-1}\$\text{S:09-804-761-1}\$\text{S:09-804-761-1}\$\text{S:09-804-761-1}\$\text{S:09-960-352-9}\$\text{S:09-960-352-9}\$\text{S:09-960-352-9}\$\text{S:09-964-761-29-91}\$\text{S:09-764-868-451-1}\$S	-09-764-878 -09-960-352- -09-864-761- 10-01-887-7 10-01-887-7 09-764-868-1 10-025-380-6 -09-833-25-217- -09-815-343- -09-815-343- -09-815-343- -09-815-343-
e 591, e 6501,	e 243, Ap e 5672, A 75, 954, A 75, Appl 111, App 683, App 683, Ap e 1683, Ap e 1683, Ap e 1683, Ap e 1683, Ap e 1684, Ap e 729, Ap

ALIGNMENTS

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Percent Similarity:
Best Local Similarity:
  Query Match:
                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of
FILE REFERENCE: 235.00440101
                                                                                                                                                                                                                                   SOFTWARE: PatentIn
                                                                                                                                                 TYPE: DNA ORGANISM: Porphyromonas gingivalis
0.363
54.00
100.00%
100.00%
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                Length:
Matches:
Conservative:
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Best Local Similarity:
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US-09-070-927A-261
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                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 261:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1930 ACGGGCGGTAACTCCGGTAGCCCCGTATTC 1959
                                                      695 ACCGGCGTCAATCTGGTTCACCAATCTAT 666
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                                                                                          1 ThrGlyGlyAsnSerGlySerProValPhe 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PB369 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/044,031 FILING DATE: 1997-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/046,655 FILING DATE: 1997-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 4951 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1-10) x US-10-008-355-1 (1-2139)
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Matches:
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Mismatches:
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; LOCATION: (1)...(450)
; OTHER INFORMATION: n =
US-09-867-701-1705
                                                  US-10-008-355-25 (1-10) x US-09-867-701-1705 (1-450)
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                                                                                                            Best Local Similarity:
Query Match:
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                                                                                                                                               Percent Similarity:
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PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 327
LENGTH: 534
TYPE: DNA
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1705
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
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TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085,500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/680,598 PRIOR FILING DATE: 2000-10-06
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                                                                                                                                                                                                                                                                                                                      FEATURE:
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; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 24-LIB34-067-Q1-E1-F7
US-09-960-352-5672
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US-09-864-761-9954/c
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US-09-764-878-243/c
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APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT FILIG NUMBER: US/09/980,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5672
LENGTH: 235
TURNEL TELLOR OF SEQ ID NOS: 15112
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SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 243
LENGTH: 7441
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APPLICANT: ROSEN et al.
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA121
CURRENT APPLICATION NUMBER: US/09/764,878
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
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ORGANISM: Homo sapiens
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; OTHER INFORMATION: MAP TO AC007463.3
OTHER INFORMATION: EXPRESSED IN HEART
OTHER INFORMATION: EXPRESSED IN BRAIT
US-09-864-761-9954
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                                                                                       US-10-008-355-25 (1-10) x US-09-864-761-9954 (1-584)
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Best Local Similarity:
Query Match:
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PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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PRIOR APPLICATION NUMBER: PCT/US01/00663
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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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3 GlyAsnSerGlySerProValPhe 10
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160 GGGAACTCTGGGACCCCCATATTT 137
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Best Local Similarity:
Query Match:
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TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and FILE REFERENCE: DEX-0269
CURRENT APPLICATION NUMBER: US/10/001,887
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/249,998
PRIOR APPLICATION NUMBER: 60/249,998
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/252,563
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin version 3.1
SEQ ID NO 75
LENGTH: 1775
TYPE: DNA
ORGANISM: Homo sapien
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APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
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SEQ ID NO 111
LENGTH: 2109
TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ32
                                                                                                                                                                                                                                                                                                                                                                          Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
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RESULT 11
US-09-922-217-683
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Best Local Similarity:
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SEQ ID NO 683
LENGTH: 3255
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Xu, Jian
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Publication No.
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
                                                                                                                                        APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
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APPLICANT:
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Stolk, John A.
Wang, Tongtong
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Smith, Carole Lynn
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Wang, Aijun
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Benson, Darin R.
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Vedvick Thomas S.
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Smith, Carole L.
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Benson, Darin R.
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                                                                                                                                                                                                                                                                                          Jiangchun
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Conservative:
Mismatches:
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APPLICANT: Wang, Aijun
APPLICANT: Clapper, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Meagher, Madeleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471012
CURRENT APPLICATION NUMBER: US/09/833, 263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 683
LENGTH: 3255
TYPE: DNA
ORGANISM: Homo sapien
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SEQ ID NO 683
LENGTH: 3255
TYPE: DNA
ORGANISM: Homo sapiens
APPLICANT: Washer, Madeleine
APPLICANT: Xu, Jiangchun
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.504
CURRENT APPLICATION NUMBER: US/09/815,343
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: FRStSEQ for Windows Version 4.0
SEQ ID NO 1415
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APPLICANT: Xu, Jiangchun

APPLICANT: King, Gordon E.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121.504

CURRENT APPLICATION NUMBER: US/09/815,343

CURRENT FILING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 1556

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 676

LENGTH: 222

TYPE: DNA

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US-09-815-343-676
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Best Local Similarity:
Query Match:
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Query Match:
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APPLICANT: Meagher, Madeleine
APPLICANT: Xu, Jiangchun
APPLICANT: King, Gordon E.
                                   SOFTWARE: FastSEQ
SEQ ID NO 1285
LENGTH: 222
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                                                                                                      TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.504

CURRENT APPLICATION NUMBER: US/09/815,343

CURRENT FILING DATE: 2001-03-22
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                                                                                         NUMBER OF SEQ ID NOS:
TYPE: DNA
ORGANISM: Homo sapien
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Maximum Match 10
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1: /cgn2_6/ptodata/1.
2: /cgn2_6/ptodata/1.
3: /cgn2_6/ptodata/1.
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Listing first 45 summaries
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US-08-523-373-23

US-08-657-192-3

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US-08-657-192-9

US-08-657-192-15

US-08-657-192-15

US-08-657-192-15

US-08-133-762A-67

US-08-332-562A-67

US-09-071-035-428

US-09-071-035-428

US-09-071-035-428

US-09-071-035-428

US-09-071-035-428

US-09-071-035-428

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US-09-071-035-428

US-09-07-61A-1

US-09-342-653-7

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US-09-144-848-22

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US-09-060-756-727
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Compugen Ltd
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; TOPOLOGY: line
; MOLECULE TYPE: F
US-08-523-373-22
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US-08-523-373-22
                                                                                                                                                                       FILING DATE: 05-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION UDATA:
APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
PRIOR APPLICATION UMBER: JP 6-296028
FILING DATE: 07-NOV-1994
PRIOR APPLICATION NUMBER: 36-6028
FILING DATE: 07-NOV-1994
APPORNEY_AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001560-25
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-6620
INFORMATION FOR SED ID NO: 22:
Query Match
Best Local S
Matches 10
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS
NUMBER OF SEQUENCES: 24
                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 699 Princ
CITY: Alexandria
STATE: VA
                                                                                                                           TYPE: amino acid
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 L Similarity
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                                                                                                                                          213 amino acids
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05-SEP-1995
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                                                                                                              not relevant
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US-08-307-279A-8
US-08-307-279A-8
US-08-307-279A-8
US-08-868-373-8
US-08-96-373-8
US-08-96-791-3
PCT-US95-10661A-3
PCT-US95-10661A-3
US-08-296-791-4
PCT-US95-10661A-4
US-08-296-791-5
PCT-US95-10661A-5
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Score 54; DB Pred. No. 0.1; Mismatches
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                               DB 3;
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                                                                                                                Sequence 24, Application US/08523373
Patent No. 6037145
GENERAL INFORMATION:
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Best Local :
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
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TELEPAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
                    APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meuth, Donna M.
REGIZATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DO
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APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN
                                                                                                                                                                                                                                                        165 TGGNSGSPVF 174
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                                                                                                                                                                                                                                                                                                                                  Local Similarity 100 es 10; Conservative
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STRANDEDNESS: not
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BURNS, DOANE, SWECKER & MATHIS
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US-08-657-192-3
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APPLICANT: YABUTA, N
APPLICANT: OHSUYE, N
TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity
Matches 10; Conserv
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                                                                                                            STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/657,192 FILING DATE: 03-JUN-1996
CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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REFERENCE/DOCKET NUMBER: 00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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TOPOLOGY: linear
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MUTANT STAPHYLOCOCCUS AUREUS V8
PROTEASES
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APPLICATION NUMBER:

JP 7-170086

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US-08-523-373-5
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: sinc
TOPOLOGY: linear
MOLECULE TYPE: prote
                                                                                                        NFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 6
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                          APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 02-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 TGGNSGSPVF 298
                                       TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                 REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC
OPERATING SYSTEM:
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                             TOPOLOGY:
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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05-SEP-1995
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                                                                                                                                                                               36,607
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                                                                                                                                                                  001560-251
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Pred. No. 0.
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Best Local Similarity
"~+~hes 10; Conserv:
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; MOLECULE TYPE: peptide
US-08-523-373-6
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US-08-523-373-6
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                                                                                         US-08-657-192-9
                                                                                                       RESULT 7
                                                            Sequence 9, Application US/08657192 Patent No. 5747321
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                                                GENERAL INFORMATION:
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    APPLICANT: YABUTA, APPLICANT: OHSUYE, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP 6-238595 FILING DATE: 07-SEP-1994 PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 703-836-6620
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                                                                                                                                                   289 TGGNSGSPVF 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/523,373 FILING DATE: 05-SEP-1995 CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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07-NOV-1994
                                                                                                                                                                                                                                                                                                              not relevant
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Kazuhiro
PROCESS FOR PRODUCTION OF PROTEIN
Masayuki
Kazuhiro
MUTANT STAPHYLOCOCCUS AUREUS V8
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Pred. No. 0.
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TITLE OF INVENTION: PROTEASES NUMBER OF SEQUENCES: 15

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LENGTH: 532 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPOLOGY: linear
MOLECULE TYPE: protein
US-08-657-192-9
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Best Local Similarity
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,192
FILING DATE: 03-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-170086
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meuth Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001560-264
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TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
TELEFAX: (705) 836-2021
INFORMATION FOR SEQ ID NO: 9:
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yabuta, Masayuki
APPLICANT: Obsuye, Kazuhiro
TITLE OP INVENTION: PROCESS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                   APPLICATION NUMBER: US/0 FILING DATE: 05-SEP-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                       STREET: 699 Princ
CITY: Alexandria
                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                           ADDRESSEE: BUKNO, L. CTREET: 699 Prince Street
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APPLICATION NUMBER:
                                                                                                                                                                                                                  ZIP: 22314-3187
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                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                            PROCESS FOR PRODUCTION OF PROTEIN
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                                                                        US/08/523,373
JP 6-238595
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Best Local Similarity
Watches 10; Conserve
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US-08-657-192-15
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; MOLECULE TYPE: US-08-657-192-15
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Patent No.
                                                                           TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 537 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-170086
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OHSUYE, TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6
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APPLICANT:
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STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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TYPE: amino acid
STRANDEDNESS: not relev
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REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 00
                               TOPOLOGY:
                                               STRANDEDNESS:
                                                                                                                                               TELEPHONE:
                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
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                                                             amino acid
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P.O. BOX 1404
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                                             single
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MUTANT STAPHYLOCOCCUS AUREUS V8
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RESULT 11
US-08-332-562A-67
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PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3729
LENGTH: 311
TYPE: PRT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 67,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/896,457
FILING DATE: 27-MAY-1992
                                                                   SOFTWARE: PatentIn Release #1.0, version #1.30 CURRENT APPLICATION DATA: APPLICATION UNMER: US/08/332,562A FILING DATE: 31-OCT-1994
                                                                                                                                   COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                      APPLICANT: BONADONNA, Lisa
APPLICANT: HULETT, Mark D.
TITLE OF INVENTION: FC RECEPTOR FOR IMMUNOGLOBULIN
NUMBER OF SEQUENCES: 136
                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 GGNSGSPVF 269
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                                                                                                                                                                                                                                                              Washington
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                                                                                                                                                                                                                                                                              E: Foley & Lardner 3000 K Street, N.W.,
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ilarity 100.0%;
Conservative 0
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                                                              31-0CT-1994
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Pred. No. 0.35;
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Best Local Similarity
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                                                                             US-09-071-035-428
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Query Match
Best Local Similarity /u.u
Thes 7; Conservative
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patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                             TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VE
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,
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CITY: R
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                                                                                                                    STRANDEDNESS:
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                                                                                                                                   amino acid
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                   Score 44; D
Pred. No. 6.
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                    Mismatches
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                                               Length 252;
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                    Indels
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Query Match
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Matches 7; Conserva
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                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: HP Vectra 486/
OPERATING SYSTEM: MSDOS:
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OFILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (301) 309-85 INFORMATION FOR SEQ ID NO:
                                                                          APPLICANT: Budtz, Peter
APPLICANT: Nielsen, Per M.
TITLE OF INVENTION: PROTEIN PREPARATIONS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 55232370 No. 5523237disk of No.
STREET: 405 Lexington Avenue, 62nd Floor
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COMPUTER READABLE FORM
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MEDIUM TYPE: Diskett
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TITLE OF INVENTION: En
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         STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
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COUNTRY:
                                                                  CITY: New York
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HP Vectra 486/33
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70.0%;
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Pred. No. 7
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                                                                                                 5523237th America, Inc
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RESULT 15
US-08-292-550-1
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Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 06-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agris, Cheryl H.
REGISTRATION NUMBER: 34,08
                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
APPLICATION NUMBER: 07/927,624
FILING DATE: 31 AUG 1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/DK91/0068
FILING DATE: 8 MAR 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
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APPLICATION NUMBER: DK 199/91
                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 GGQSGSPVF 172
                                                                                                                         APPLICATION NUMBER: FILING DATE: 18 AUCCLASSIFICATION: 42
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                                                                                                                                                                                                                                                                                                                         STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 16-JU CLASSIFICATION: 43
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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nes 8; Conserv
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A PROCESS FOR PRODUCING CHEESE
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -Q=/cgn2_1/USPTO_spool/US10008355/runat_17122002_112338_14609/app_query.fasta_1.398
-DB=EST -QFMT=fastap -SUFFIX=P2n.rst -MINATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MARTRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -AMXLEN=200000000
-USER-US1000835_@CCM_1_1_763_@runat_17122002_112338_14609 -NCPU=6 -ICPU=3
-NO_MARP_TIMEOUT=30 -THREADS=1 -NOAPOP=10 -NOAPDEXT=0.5 -FGAPDP=6 -FGAPEXT=7
-YGAPDP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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-MODEL=frame+_p2n.model -DEV=xlh
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AA411980/c	RESULT 1	
17.2 7 7 2 2 2 2	1 (base	Mammalia	Eukaryot	Homo sap	human.	EST.	AA411980	AA411980	3', mRNA	zt65g03.	AA411980			

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 318)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B. 318 soares_testis_NHT iens 'n sequence. GI:2070632 bp mRNA Homo sapiens linear E EST 12-AUG-1997 e IMAGE:727252

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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGGGAGGAAACTCTGGCAGTCCTATT 193
Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J. Direct Submission of BAC-end sequences from Anopheles gambiae Unpublished (2001) Other_GSSs: AG-ND-147H4.TR Contact: Brendan J Loftus Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                            Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                            DNA sequence
BH400391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infoimage.llnl.gov) for further information. Insert Length: 2072 Std Error: 0.00 Seq primer: -41m13 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU.Merck EST Project 1997
                                                                                                                                                                                                                                                                African malaria mosquito.
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/db_xref="GDB:5924164"
/db_xref="taxon:9606"
/clone="IMAGE:727252"
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                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 608)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N.,
M., Konno,H., Okazaki,Y., Muramatsu,
                                                                                                                                                           Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTS (Arakawa,T., et al. 2001)

Unpublished (2001)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap

Tel: 81-45-503-9222
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This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University. College Station, Texas 77843-2123, USA using a HindIII
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                                                                                                                                        Fax: 81-45-503-9216
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., I:M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           608 bp mRNA linear EST 26-OCT-2001 RIKEN full-length enriched, adult male olfactory brain Mus cDNA clone 6430525L24 5', mRNA sequence.
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/note="Vector: pECBAC1; Site_1: HindIII"
79 c 76 g 160 t
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/clone="AG-ND-147H4"
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                                                                                                                                                  TCTGGTGGAAATTCTGGAAACCCAGTTTTT 590
 mRNA sequence.
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                                 BF694219 611 bp mRNA linear EST 22-D 602082842F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Salto, T., Kiyosawa, H., Yemanaka, I., Aizav, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watahiki,M.,
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e mouse tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computer-based methods for the mouse full-length cDNA
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i,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., hiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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/clone="6430525L24"
/clone_lib="RIKEN full-length enriched, adult male olifactory brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepared and sequenced in Mouse Genome Encyclopédia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="olfactory brain"
/dev_stage="adult"
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KEYWORDS
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                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 371)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
                                                                                                                                                                                                                                                                                                              AQ699991 371 bp DNA linear HS_5334_A2_G04_SP6E RPCI-11 Human Male BAC Library genomic clone Plate=910 Col=8 Row=M, DNA sequence.
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1063 row: d column: 12
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NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection () Unpublished (1999)
Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                           genomic clone
AQ699991
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Tissue Procurement: CLONETECH Laboratories,
                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NIH_MGC_01"
/lab_host="DH10B (T1 phage-resistant)"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
/clontech); Site_1: SfiI (9gccgctcggcc); Site_2: SfiI
(9gccattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTACAGGCCGACGCCGCACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T]. Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
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/db_xref="taxon:9606"
/clone="IMAGE:4247003"
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Tex: (206) 616-3687
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (lifo@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
                                                                                                                                 1 (bases 1 to 497)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Baia, G.S., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                       BQ327884
BQ327884.1 GI:20945640
EST.
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MR4-RT0045-250401-009-g06 RT0045 Homo sapiens
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Location/Qualifiers
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Proc. Natl. Acad. Sci. U.:
99380589
                    Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Seq primer: SP6
Laboratory of Cancer Genetics
                                                                            sequence tags
                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen do and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

88 c 79 g 117 t
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/db_xref="taxon:9606"
/clone="Plate=910 Col=8 Row=M"
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ncing Center
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AUTHORS
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BG714149/c
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source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
BG714149
BG714149.1 GI
                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shira
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 796)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Seq primer: puc 18 forward
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602674594F1 NIH_MGC_96 Homo
                 High quality sequence stop: 677.
Location/Qualifiers
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High quality sequence stop: 37.
Location/Qualifiers
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Fax: +55-11-2707001
                                                                   http://image.llnl.gov
Plate: LLAM10682 row: l column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue mRNA and cDNA amplification were performed under low stringency conditions."

164 c 176 g 102 t 1 others
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/dev_stage="Adult"
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/db_xref="taxon:9606"
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Mismatches:
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                                                                                                                                                                                                                                    (NHGRI), Shiraki
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US-10-008-355-25 (1-10) x BG714149 (1-796)
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                                                                                                                                                                                                                                                                                                              Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                          http://image.llnl.gov
Plate: LLCM893 row: m column:
High quality sequence stop: 647.
                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:4797094"
/clone_lib="NIH_MGC_96"
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/db_xref="taxon:9606"
                                                                                                                                               /clone="IMAGE:4054078"
/clone_lib="NIH_MGC_48"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="hypothalamus"
/lab_host="DH10B"
                                                                                                                                                                                     organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                           Location/Qualifiers
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Query Match:

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Pred. No.: Alignment Scores: BASE COUNT

BF128636 RESULT 8

REFERENCE AUTHORS TITLE

SOURCE

ORGANISM

KEYWORDS VERSION ACCESSION DEFINITION

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US-10-008-355-25 (1-10) x BF128636 (1-914)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
BG115436
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:4416831"
/clone=lib="NIH_MGC_88"
/clone=lib="NIH_MGC_88"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
/note="Organ: small intestine; pCMV-SPORT6;
/note="Organ: pCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV1&t2=QV1-MT0166-
131100-476-b02&t3=2000-11-13&t4=1)
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Ludwig Institute for Cancer Research
AW060086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence tags
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prof. Antonio Prudente 109, 4 andar, 01509-010,
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/db_xref="taxon:9606"
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                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Tel: 650 723 2227
Fax: 650 725 8251
Email: walbot@stanford.edu
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1 (bases 1 to 279)
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/db_xref="taxon:4577"
/clone_lib="687 - Early embryo from Delaware"
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RESULT 13
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                                                                                               The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                         Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 403)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.
              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information
                                                                    Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                  AA476126 403 bp mRNA linear vh17d08.rl.Soares_mammary_gland_NbMMG Mus musculus IMAGE:875727 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kitayama, A., Terasaka, C., Mochii, M., Ueno, N.,
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Location/Qualifiers
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72 c 62 g 58 t 4 others
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/db_xref="taxon:8355"
/clone="XL155108"
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/dev_stage="stage 10.5"
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Contact: Wilson RK
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1 (bases 1 to 420)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             zd60g08.sl Soares.fetal_heart_NbHH19W Homo sapiens IMAGE:345086 3', mRNA sequence.
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                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. J
Tel: 314 286 1800
Fax: 314 286 1810
High quality sequence stop: 325.
Location/Qualifiers
                                             Seq primer: mob.REGA+ET
                                                                       This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i Insert Length: 389 Std Error: 0.00
                                                                                                                                                       Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

86 g 141 t
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/lab_host="DH10B"
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/clone="IMAGE:875727"
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/strain="C57BL/6J"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 432)
1 (bases 1 to 432)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AW743569 AW743569.1 GI:7655383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI:1053865
Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
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/
                         /db_xref="taxon:10090"
/clone="IMAGE:3025157"
                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
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/db_xref="GDB:1270461"
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/dev_stage="19 weeks"
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double-stranded cDNA was ligated to Eco RI adaptors
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ORIGIN

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RESULT 15

FOCUS. AW743569

VERSION ACCESSION

KEYWORDS

TITLE

FEATURES

Alignment S Pred. No.: US-10-008-355-25 (1-10) x AW743569 (1-432) Percent Similarity: Best Local Similarity: Query Match: Score: ORIGIN BASE COUNT 125 מ (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

96 g 134 t 100.00% 88.89% 81.48% 1.04e+03 44.00 Gaps: Indels: Mismatches: Conservative:

Search completed: December 20, Job time: 1535.05 secs 2002, 15:48:51

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A_Geneseq_101002:*

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Copyright (c) 1993 - 2002 Compugen Ltd
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52
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V8 mature protease
V8 mature protease
V8 mature protease
Protease from S. A
Beta-galactosidase
Protein encoded by
Protease from S. A
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Porphyromonas ging
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V8 mature protease
V8 mature protease
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ALIGNMENTS

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RESULT 1
                                    WPI; 2002-490075/52.
                                                                                                                                                                                                Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; active site; DPP-7 inhibitor identification; periodontal disease; gingivitis; periodontitis.
                                                       Travis J,
                                                                                                                  08-NOV-2001; 2001WO-US46782
                                                                                                                                                                     Porphyromonas gingivalis.
                                                                                                                                                                                                                                      Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) active site
                                                                                                                                                                                                                                                           05-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                   AAO15228 standard; Peptide; 10 AA
                                                                                               08-NOV-2000; 2000US-246827P.
                                                                                                                                       16-MAY-2002.
                                                                                                                                                           WO200238742-A2.
                                                                                                                                                                                                                                                                                AAO15228;
                                                                           (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                       Potempa JS,
                                                       Banbula A,
                                                       Bugno
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AAR26842

Novel isolated dipeptidylpeptidase useful for identifying inhibitor of the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis $\,$

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RESULT 2
AAO15206
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Best Local
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The invention comprises the amino acid and coding sequence of the PP-7 Porphyromonas gingivalis dipeptidylpeptidase 7 (PPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidglepptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents an active site region of the Porphyromonas gingivalis dipeptidylepptidase-7 (DPP-7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                Novel isolated dipeptidylpeptidase useful for identifying inhibitor the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; gingi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAO15206 standard;
                                                                                                                                                                   Example 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porphyromonas gingivalis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                               ۶,
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                                                                                                                                                                                                                                                                                               Bugno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 23;
0.031;
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TGGNSGSPVF

Similarity

Conservative

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Mismatches

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Indels

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0.17;

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Query Match
Best Local S
Matches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                            The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidylpeptidase-7 (PPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents the C-terminal region of the Staphylococcus aureus V8 endopeptidase enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C-terminal region of the Porphyromonas (DPP-7) enzyme.
                                                                                                                                                                                                                                                                                           Novel isolated dipeptidylpeptidase useful for identifying inhibitor the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; gingi periodontitis; V8 endopeptidease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents the C-terminal region of the Porphyromonas gingivalis dipeptidylpeptidase-7
                                                      Sequence
                                                                                                                                                                                                                                                                   Example 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-2001; 2001WO-US46782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200238742-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAO15207 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                             (UYGE-) UNIV GEORGIA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAO15207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TGGNSGSPVF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGNSGSPVF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
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                                                                                                                                                                                                                                                                  Fig 5; 65pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
                                                      52
                                                                                                                                                                                                                                                                                                                                                                                 Potempa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-246827P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ĀΑ;
                                                      AΑ;
                                                                                                                                                                                                                                                                                                                                                                                   JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                   Banbula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 54;
Pred. No.
             Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                Bugno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-terminal region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽B
                           DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                        Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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TGGNSGSPVF 10

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RESULT 5
AAR91043
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AAR91042
  DEXTXACXI
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                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                         A fusion protein, V8D (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides, B is Staphylococcus aureus mature V8 protease lacking the C-terminal repeat region, and L is a linker (AAR91032). It was produced as an inclusion body in Escherichia coli host cells, and was cleaved using the E. coli OmpT protease to yield active V8 protease. Extension of the C-terminal end of the V8 moiety of the fusion protein by 1, 2 or 3 amino acids (AAR91042-44) i.e. up to residue Phe-215, also resulted in the formation of inclusion bodies in E. coli. Any further extension gave a soluble product which exhibited protease activity that repressed growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                              Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Linker peptide; V8 protease; Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escherichia coli; transposon Tn903; aminoglycoside 3'-phosphotransferase.
  8
                          23-MAY-1996
                                                                          AAR91043 standard;
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       Example 8; Fig 14a; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-141021/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP700995-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus strain V8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V8 mature protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR91042 standard; Peptide; 213 AA.
                                                                                                                                         165 TGGNSGSPVF 174
mature protease (aal-214)
                                                                                                                                                       1 TGGNSGSPVF 10
                                                                                                                                                                                                                                                                    host cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ~
                                                                                                                                                                                          10;
                                                                                                                                                                                                                                            213 AA;
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94JP-0296028.
94JP-0238595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95EP-0306235
                                                                          Peptide; 214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (aa1-213)
                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                          0
                                                                                                                                                                                                    Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ATCC
                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27733)
                                                                                                                                                                                                    0.73;
                                                                                                                                                                                                                DB 17;
                                                                                                                                                                                          0
                                                                                                                                                                                                                Length 213;
                                                                                                                                                                                          Indels
                                                                                                                                                                                          0
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RESULT 6
AAR91044
QУ
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                        A fusion protein, V8D (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides, B is Staphylococcus aureus mature V8 protease lacking the C-terminal repeat region, and L is a linker (AAR91032). It was produced as an inclusion body in Escherichia coli host cells, and was cleaved using the E. coli OmpT protease to yield active V8 protease. Extension of the C-terminal end of the V8 moiety of the fusion protein by 1, 2 or 3 amino acids (AAR91042-44) i.e. up to residue Phe-215, also resulted in the formation of inclusion bodies in E. coli. Any further extension gave a soluble product which exhibited protease activity that repressed growth of
                                                                                              Linker peptide; V8 protease; Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escherichia coli; transposon Tn903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombinant protein; fusion protein; beta-galactosidase; Escherichia coli; transposon Tn903; aminoglycoside 3'-phosphotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohsuye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-NOV-1994;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus strain V8 (ATCC 27733).
                                                             Staphylococcus
                                                                                     aminoglycoside
                                                                                                                                                      V8 mature protease (aal-215).
                                                                                                                                                                                23-MAY-1996
                                                                                                                                                                                                          AAR91044;
                                                                                                                                                                                                                                  AAR91044 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 8; Fig 14b; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP700995-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Linker peptide; V8 protease; Staphylococcus aureus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                ||||||||||
165 TGGNSGSPVF 174
                                                                                                                                                                                                                                                                                                                          1 TGGNSGSPVF
                                                                                                                                                                                                                                                                                                                                                                                                                                 host cells.
                                                                                                                                                                                                                                                                                                                                                    10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                        214 AA;
                                                                                  protein; fusion protein; coli; transposon Tn903; ide 3'-phosphotransferase.
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94JP-0296028.
94JP-0238595.
                                                             aureus strain V8 (ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95EP-0306235
                                                                                                                                                                                                                                                                                                                            10
                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                   215
                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                Score 54;
Pred. No.
                                                                                                                                                                                                                                  AA
                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                             27733)
                                                                                                                                                                                                                                                                                                                                                                DB 17;
0.73;
                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                              214;
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RESULT 7
AAR29644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A fusion protein, V8D (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides, B is Staphylococcus aureus mature V8 protease lacking the C-terminal repeat region, and L is a linker (AAR91032). It was produced as an inclusion body in Escherichia coli host cells, and was cleaved using the E. coli OmpT protease to yield active V8 protease. Extension of the C-terminal end of the V8 molety of the fusion protein by 1, 2 or 3 amino acids (AAR91042-44) i.e. up to residue Phe-215, also resulted in the formation of inclusion bodies in E. coli. Any further extension gave a soluble product which exhibited protease activity that repressed growth of
          N-PSDB; AAQ27988
                                                                                                                                                                                                                       Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohsuye K,
                    WPI; 1992-304938/37.
                                                                                                            03-AUG-1992.
                                                                                                                                 JP04211370-A.
                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                           11-FEB-1993
                                                                                                                                                                                                                                                                                                                 AAR29644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-NOV-1994;
07-SEP-1994;
                                                                 20-FEB-1990;
                                                                                      19-FEB-1991;
                                                                                                                                                                                                                                             Protease;
                                                                                                                                                                                                                                                                     Protease from
                                                                                                                                                                                                                                                                                                                                     AAR29644 standard; Protein; 336 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 8; Fig 14c; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-SEP-1995;
                                         (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                             165
                                                                                                                                                                                                                                                                                                                                                                                                       1 TGGNSGSPVF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          host cells.
                                                                                                                                                                                                                                                                                                                                                                                             TGGNSGSPVF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
10; Conserv
                                                                                                                                                                                                                                             PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ĀΑ;
                                                                 90JP-0040398
                                                                                                                                                                                                                         aureus
                                                                                                                                                                                                                                             amplify; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94JP-0296028
94JP-0238595
                                                                                      91JP-0024633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95EP-0306235
                                                                                                                                                                  /label= Signal_peptide
69..336
                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                       /label= Protease
                                                                                                                                                                                                                                                                     Aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              215;
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RESULT 8
AAR91033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
Fusion proteins (AAR91033 and AAR91034) were constructed comprising an Escherichia coli beta-galactosidase derivative (protective polypeptide) fused at its C-terminal end to the S. aureus mature V8 protease without or with the repeat region. The constructs were inserted into vector pG97S4DhCT(G)R6, yielding pV8RPT(-) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAR26842 and AAR29644 are proteases which we isolated from Staphylococcus aureus strains. The DNA sequences encoding these proteins were isolated by PCR using the primer sequences given in AAQ27960-86. The protease specifically cleaves the peptide bond at the C-terminus of the glutamic acid residue in polypeptide.
                                                                                                         Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective
                                                                                                                                                                                                                       07-NOV-1994;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric Staphylococcus aureus strain V8
                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel protease prepd. using Bacillus or Saccharomyces host capable of cleaving peptide bond at carboxyl terminus of glutamic acid residues in polypeptide(s)
                                                                         Example 2; Page 12-13; 44pp; English.
                                                                                                                                                                       Ohsuye K,
                                                                                                                                                                                                                                                          06-SEP-1995;
                                                                                                                                                                                                                                                                                                         EP700995-A2
                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beta-galactosidase-V8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR91033 standard; Protein; 344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 15-16;
                                                                                                                                                                                                                                                                                  13-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V8 protease; Staphylococcus aureus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR91033;
                                                                                                                                                                                               (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 TGGNSGSPVF 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TGGNSGSPVF 10
                                                                                                                                                  1996-141021/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli;
                                                                                                                                                                       Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŘΑ;
                                                                                                                                                                                                                       94JP-0296028
94JP-0238595
                                                                                                                                                                                                                                                          95EP-0306235
                                                                                                                                                                                                                                                                                                                                                         /note= "beta-galactosidase 125..344
                                                                                                                                                                                                                                                                                                                                                                                                                                                      beta-galactosidase;
                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protease
                                                                                                                                                                                                                                                                                                                                25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        recombinant
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                   (ATCC 27733)
                                                                                                                                                                                                                                                                                                                                                                   region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336;
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      The invention relates to new mutant staphylococcus aureus V8 proteases which have enzyme activity even under environmental conditions which promote protein denaturation. The mutants are based on 3 truncated V8 proteases lacking 48 (AAW22218), 56 (AAW22219) or 53 (AAW22220) amino acids from the C-terminal of the wild type protease. The mutants also contain amino acid substitutions, especially D44E, N71S and/or R147K. The protein sequence shown here represents a chimaeric protein comprising a truncated Staphylococcus aureus V8 protease lacking the prepro and C-terminal 48 amino acids linked, via a synthetic linker, downstream of the E. coli beta-galactosidase. The S. aureus portion of the chimaera was amplified by the primers AAT73254-5 from wild type sequence. The coding sequence was then used to generate mutants of the V8 protease which retain their levels of activity in the presence of a chimaera concentration of protein denaturant e.g. 5 M urea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Region
                                                                                                                                                                                                                                          Claim 2;
                                                                                                                                                                                                                                                                                      Staphylococcus aureus V8 protease mutants - with
                                                                                                                                                                                                                                                                                                                                                Ohsuye K,
                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mutant; Staphylococcus aureus; V8 protease; enzyme; denaturation; primer; truncation; wild type; PCR; polymerase chain reaction; amplification; proteolytic activity; fusion protein; beta-galactosidase; urea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by pV8RPT(-) construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW22218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW22218 standard; Protein; 344 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \ensuremath{\mathsf{PV8RPT(+)}}\xspace , respectively. Both constructs yielded active protease when expressed in E. coli JM101 transformants.
                                                                                                                                                                                                                                                                      resistance to denaturation
                                                                                                                                                                                                                                                                                                                                                                              (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP745669-A2
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                                                                                                                                                                                                                                                                                                                    1997-013693/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGNSGSPVF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity 100 10; Conservative
                                                                                                                                                                                                                                      Page 13-14; 42pp; English
                                                                                                                                                                                                                                                                                                                                                Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           95JP-0170086
                                                                                                                                                                                                                                                                                                                                                                                                                                           96EP-0303939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "truncated S. aureus V8 protease portion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101..120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "E. coli beta-galactosidase portion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "synthetic R6 linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB
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                                                                                                                                                                                                                                                                                    increased
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RESULT 11
AAR91034
ID AAR91
XX
AC AAR91
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AAR26842
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                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                 The sequences given in AAR26842 and AAR29644 are proteases which were isolated from Staphylococcus aureus strains. The DNA sequences encoding these proteins were isolated by PCR using the primer sequences given in AAQ27960-86. The protease specifically cleaves the peptide bond at the C-terminus of the glutamic acid residue in polypeptide.
 AAR91034;
                   AAR91034 standard; Protein; 392 AA
                                                                                                                                                                                                                                                          Novel protease prepd. using Bacillus or Saccharomyces host capable of cleaving peptide bond at carboxyl terminus of glutamic acid residues in polypeptide(s)
                                                                                                                                                                                                                                                                                                    WPI; 1992-304938/37.
N-PSDB; AAQ27987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                 Sequence
                                                                                                                                                                                                                                       Disclosure; Page 13-15;
                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                JP04211370-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR26842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR26842 standard; Protein; 357
                                                                                                                                                                                                                                                                                                                                                     20-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protease; PCR; amplify; Staphylococcus
                                                                                                                                                                                                                                                                                                                                (SHIO ) SHIONOGI & CO
                                                                                                                                                                                                                                                                                                                                                                       19-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                    233 TGGNSGSPVF 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 TGGNSGSPVF 298
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                                                                                      1 TGGNSGSPVF 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                                                                                                                                  357
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                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S. Aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                  AΑ;
                                                                                                                                                                                                                                                                                                                                                     90JP-0040398
                                                                                                                                                                                                                                                                                                                                                                         91JP-0024633
                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Signal_peptide
69..358
                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                  100.0%;
                                                                                                                                                                                                                                        25pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCC12600
                                                                                                           0;
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                                                                                                                 Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54; DE
Pred. No. 1.2
0; Mismatches
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                                                                                                          Mismatches
                                                                                                                  DB :
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                                                                                                                             13;
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                                                                                                                             Length 357;
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                                                                                                                RESULT 12
                                                                                                                                                                        Query Match
Best Local S
Matches 10
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Chimeric
                                                                                                                                                                                                                      Fusion proteins (AAR91033 and AAR91034) were constructed comprising an Escherichia coli beta-galactosidase derivative (protective polypeptide) fused at its C-terminal end to the S. aureus mature V8 protease without or with the repeat region. The constructs were inserted into vector pg97S4DhCT(G)RG, yielding pv8RPT(+) and pv8RPT(+), respectively. Both constructs yielded active protease when expressed in E. coli JM101 transformants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Region
     Linker peptide; V8 protease; Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escherichia coli; transposon Tn903; aminoglycoside 3'-phosphotransferase.
                                               Recombinant V8
                                                               23-MAY-1996
                                                                               AAR91035
                                                                                              AAR91035 standard; Protein;
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                       Example 2; Page 14-15; 44pp; English.
                                                                                                                                                                                                                                                                                                        polypeptide
                                                                                                                                                                                                                                                                                                              Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective
                                                                                                                                                                                                                                                                                                                                        WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                        Ohsuye K,
                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-1994;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP700995-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V8 protease; fusion prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beta-galactosidase-V8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                        (SUNR ) SUNTORY LTD
                                                                                                                                         289
                                                                                                                                                        ب
                                                                                                                                         TGGNSGSPVF 298
                                                                                                                                                        TGGNSGSPVF 10
                                                                                                                                                                       ch 100.0%; l Similarity 100.0%; 10; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tease; Staphylococcus aureus;
protein; beta-galactosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli;
Staphylococcus au
                                                                                                                                                                                                         392
                                                                                                                                                                                                                                                                                                                                                        Yabuta M;
                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                         AA;
                                               protease V8D
                                                                                                                                                                                                                                                                                                                                                                                         94JP-0296028.
94JP-0238595.
                                                                                                                                                                                                                                                                                                                                                                                                                 95EP-0306235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
125..39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protease fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "mature V8 protease including the repeat region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "beta-galactosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aureus strain
                                                                                               532
                                              fusion protein.
                                                                                                                                                                        0;
                                                                                                                                                                      Score 54; DB 1
Pred. No. 1.4;
0; Mismatches
                                                                                               AA
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Escherichia
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RESULT 13
AAW22219
ID AAW22
XX
AC AAW22
XX
DT 11-SE
XX
DE Prote
                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                 A fusion protein, V8D (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides (derived from Escherichia coli beta-galactosidase and and Tn903 aminoglycoside 3'phosphotransferase, respectively), B is Staphylococcus aureus mature V8 protease lacking the C-terminal repeat region, and L is a linker peptide (AAR91032). The fusion protein is expressed in inactive form in E. coli. It is then recovered, solubilised and cleaved at the linker peptide regions with a protease intrinsic to the host cells, i.e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric Chimeric Chimeric Chimeric Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Region
                                  11-SEP-1997
                                                                  AAW22219;
                                                                                                AAW22219 standard; Protein;
                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 16-18; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohsuye K, Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-1994;
07-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-1995;
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                                                                                                                                                                               289
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                                                                                                                                                                               TGGNSGSPVF 298
                                                                                                                                                                                                           TGGNSGSPVF 10
                                                                                                                                                                                                                                                                                                                                        protease, to allow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUNTORY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli;
synthetic;
staphylococcus aureus strain
transposon Tn903.
                                                                                                                                                                                                                                                                                                           532 AA;
                                                                                                                                                                                                                                            Conservative
                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94JP-0296028.
94JP-0238595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95EP-0306235
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339..340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "beta-galactosidase
101..120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125..335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
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                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "R6 linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "cleavage site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "aminoglycoside 3'phosphotransferase
region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "V8 protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "R6 linker"
                                                                                                                                                                                                                                                                                                                                      recovery of V8
                                                                                                 532
                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                          Score 54; DB
Pred. No. 1.9;
                                                                                                 A
                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for OmpT
                                                                                                                                                                                                                                                                                                                                        protease.
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                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease"
                                                                                                                                                                                                                                                                         Length 532;
                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                            Gaps
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Protein encoded by pV8D construct.

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RESULT 14
AAW22220
                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to new mutant Staphylococcus aureus V8 proteases CC which have enzyme activity even under environmental conditions which CC promote protein denaturation. The mutants are based on 3 truncated V8 CC proteases lacking 48 (AAW22218), of 5 (AAW22219) or 53 (AAW22220) amino CC contain amino acid substitutions, especially D44E, N715 and/or R147K. CC The protein sequence shown here represents a chimaeric protein CC comprising a truncated Staphylococcus aureus V8 protease lacking the CC prepro and C-terminal 56 amino acids linked, via a synthetic R6 linker, CC downstream of the E. coli beta-galactosidase. Also included downstream of the Protease fragment is a second R6 linker and a fragment of the CC aminoglucoside 3'-phosphotransferase protein. The chimaeric sequence CC was generated by restriction digestion and ligation from the V8RPT(-) CC sequence (see AAW22218) by using a natural EcoRV site which removed a CC further 8 amino acid from the C-terminus. This truncated V8 protease, cold designated V8D, retains its level of activity in the presence of a cc higher concentration of protein denaturant e.g. 5 M urea.
                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                             Query Match
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Chimeric
AAW22220;
                                            AAW22220 standard; Protein; 537 AA.
                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus V8 protease mutants - with increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-013693/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohsuye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutant; Staphylococcus aureus; V8 protease; enzyme; denaturation; primer; truncation; wild type; PCR; polymerase chain reaction; amplification; proteolytic activity; fusion protein; beta-galactosidase; urea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                resistance
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                                                                                                                                                                              289
                                                                                                                                                                                                                                                                           Local Similarity
mes 10; Conserv
                                                                                                                                                                                                                           1 TGGNSGSPVF 10
                                                                                                                                                                           TGGNSGSPVF 298
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                                                                                                                                                                                                                                                                                                                                                                               532 AA;
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Staphylococcus aureus.
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/note= "R6 linker sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "E. coli beta-galactosidase portion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
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                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                     Length 532;
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RESULT 15

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The invention relates to new mutant Staphylococcus aureus V8 proteases CC which have enzyme activity even under environmental conditions which CC promote protein denaturation. The mutants are based on 3 truncated V8 proteases lacking 48 (AAW22218), 56 (AAW22219) or 53 (AAW22220) amino CC acids from the C-terminal of the wild type protease. The mutants also contain amino acid substitutions, especially D44E, N71S and/or R147K. The protein sequence shown here represents a chimaeric protein CC comprising a truncated Staphylococcus aureus V8 protease lacking the preprior and C-terminal 53 amino acids linked, via a synthetic R6 linker, CC downstream of the E. coli beta-galactosidase. Also included downstream of the V8 protease fragment is a second R6 linker and a fragment of the C aminoglucoside 3'-phosphotransferase protein. The chimaeric sequence was generated by restriction digestion and ligation from the V8RPT(-) CC sequence (see AAW22218) by using a natural EcoRV site which removed a further 8 amino acid from the C-terminus. This truncated V8 protease, designated V8F, retains its level of activity in the presence of a higher concentration of protein denaturant e.g. 5 M urea.
                                                                                                         Matches
                                                                                                                                  Query Match
Best Local :
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                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohsuye K, Yabuta M;
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289 TGGNSGSPVF 298
                                                                                                                                  Local Similarity
                                                    1 TGGNSGSPVF 10
                                                                                                         10;
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                                                                                                                                                                                                               537 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus.
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                                                                                                100.0%; ilarity 100.0%; Conservative
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101..124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "R6 linker sequence"
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                                                                                                                               Score 54; DB Pred. No. 1.9;
                                                                                                      Mismatches
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                                                                                                                       Best Local Similarity Matches 10; Conserv
                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                           The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidyse? (DPP-7) enzyme. The DP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme of the
                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Fig 4; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated dipeptidylpeptidase useful for identifying inhibitor of the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Travis J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-NOV-2000; 2000US-246827P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         periodontitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7).
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GenCore version 5.1.3 (c) 1993 - 2002 Compugen Ltd
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RESULT 2
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hypothetical protein sspA [imported] - Staphylococcus
C; Species: Staphylococcus aureus
C; Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: G89873
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
R;Kuroda, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
rancet 357, 1225-1240, 2001

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1 TGGNSGSPVF 10 TGGNSGSPVF 242

233

Query Match Best Local : Matches

Local 5.

Similarity

100.0%; 5 100.0%; F tive 0;

Score 54; DB 1 Pred. No. 0.13; Mismatches

DB 1; 0;

Length 336; Indels

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Gaps

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Conservative

C;Superfamily: staphylococcal serine proteinase C;Keywords: hydrolase; serine proteinase F;69-336/Product: staphylococcal serine proteinase #status experimental <act>F;119,161/Active site: His, Asp #status predicted F;237/Active site: Ser #status experimental</act>	otein 110-124;126-144,'D',146-192,'T',194-228,'N',230-258,'Q', ce: strain V8 racellular proteolytic enzyme preferentially cleaves the yme may be distantly related to the trypsin-type serine	A;Molecule type: DNA A;Residues: 1-336 <car> A;Cross-references: EMBL:Y00356; NID:g46686; PIDN:CAA68434.1; PID:g46687 A;Experimental source: strain V8 R;Drapeau, G.R. Can. U. Biochem. 56, 534-544, 1978 A;Title: The primary structure of staphylococcal protease. A;Reference number: A23824; MUID:78212487; PMID:96922</car>	glutamyl endopeptidase (EC 3.4.21.19) precursor - Staphylococcus aureus N;Alternate names: staphylococcal serine proteinase C;Specias: Staphylococcus aureus C;Date: 04-Dec-1986 #sequence_revision 30-Jun-1991 #text_change 18-Jun-1999 C;Accession: A26812; A00966 R;Carmona, C: Gray, G.L. Nucleic Acids Res. 15, 6757, 1987 Nucleic Acids Res. 15, 6757, 1987 A;Title: Nucleotide sequence of the serine protease gene of Staphylococcus aure A;Reference number: A26812; MUID:87316953; PMID:3306605 A;Accession: A26812	ALIGNMENTS RESULT 1 PRSASK	30 37 68.5 449 2 B71265 31 37 68.5 462 2 H97292 32 37 68.5 590 2 AB1411 33 37 68.5 817 2 T21336 34 37 68.5 1254 2 T47141 36 37 68.5 1254 2 T47141 37 68.5 1306 2 A70934 38 36 66.7 280 2 T28684 40 36 66.7 374 2 T09111 41 36 66.7 374 2 T09111 42 36 66.7 411 2 T15209 43 36 66.7 425 2 D64149 44 36 66.7 425 2 D64149 45 36 66.7 493 2 C97605
<act></act>	'Q',260,'D',26 the peptide b		1999 Tus aureus, st		tran nuramo prote prote glyci prote

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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.
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A; Molecule type: DNA
A; Residues: 1-342 < KUR>
A; Cross-references: GB:BA000018; PID:g13700850;
                                                                                                                                                                                                       A:Molecule type: DNA
A:Residues: 1-716 <SIM>
A:Cross-references: GB:AE004008; GB:AE003849; NID:g9106961; PIDN:AAF84693.1; GSPDB:GN00:
A:Experimental source: strain 9a5c
                                                                                                                                                                                                                                                                                                                                           A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein XF1887 [imported] - Xylella fastidiosa (strain c;SpecLes: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-AC;Accession: G82627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA A;Residues: 1-357 <YOS>
A;Residues: 1-357 <YOS>
A;Cross references: GB:D00730; NID:g216970; PIDN:BAA00630.1; PID:g216971 C;Superfamily: staphylococcal serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;YOShikawa, K.; Tsuzuki, H.; Fujiwara, T.; Nakamura, E.; Iwamoto, H.; Matsumoto, K.; S: Blochim. Blophys. Acta 1121, 221-228, 1992
A;Title: Purification, characterization and gene cloning of a novel glutamic acid-speci A;Reference number: S21758; MUID:92287954; PMID:1599945
A;Accession: S21758
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glutamic acid-specific endopeptidase - Staphylococo (;Species: Staphylococcus aureus C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 C;Accession: S21758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Accession: G89873
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A; Status: preliminary
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C;Superfamily: staphylococcal serine
                                                                                                                                                                                                                                                                                                                                                                                                               R; anonymous, The Xylella fastidiosa Consortium Nature 406, 151-157, 2000\,
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10; Conserv
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Pred. No.
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Pred. No. 0.13;
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submitted to the EMBL Data Library, June A;Description: A gene (sprE) downstream c A;Reference number: S25140 A;Accession: S25140
A;Status: preliminary
A;Molecule type: protein
A;Residues: 95-316 <SVE>
C;Keywords: hydrolase
                                                                               A; Reference number: S23078;
A; Accession: S23078
                                                                                                                                                        A;Note: sequence extracted from NCBI backbone (NCBIN:118784, R;Svendsen, I.; Breddam, K.
                                                                                                                                                                                               A;Cross-references: GB:D10060; NID:g216263; PIDN:BAA00949.1; A;Experimental source: ATCC 14580
                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-316 <KAK>
                                                                                                                                                                                                                                                                                               J. Biol. Chem. 267, 23782-23788, 1992
A;Title: Purification, characterization, cloning, and expression A;Reference number: A45134; MUID:93054737; PMID:1429718
A;Accession: A45134
                                                                                                                                                                                                                                                                                                                                                                                            endopeptidase (EC 3.4.--), glutamate-specific - Bacillus licheniformis C;Species: Bacillus licheniformis C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999 C;Accession: A45134; S23078
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A; Residues: 1-284 <SUY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Species: Enterococcus faecalis
C:Date: 20-Feb-1995 #sequence_revision
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                                                                                                                      A; Title: Isolation and amino acid
                                                                                                                                                                                                                                                                          A; Status: preliminary
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                      S.; Kikuchi, N.; Kitadokoro,
Chem. 267, 23782-23788, 1992
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                                                                                                 o acid sequence
MUID:92155199;
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Silva, F.R.; da Silva, A.M.; Silva Jr.,
Van Sluys, M.A.; Verjovski-Almeida, S.;
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Pred. No.
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Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-Feb-1995
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                                                                                                                                                                                                                     PID:d1001415;
                                                                                                                                                                             NCBIP:118785)
                                                                                                                      specific endopeptidase
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lva Jr., W.A.; da
ida, S.; Vettore,
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Similarity 8; Conser

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Score 43; DB Pred. No. 8.5; 0; Mismatches

DB 3.5;

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Length 316;

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88

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A;Molecule type: DNA
A;Residues: 1-50 <HTL>
A;Cross-references: EMBL:U43738
A;Cross-references: EMBL:U43738
R;Himmelraich, R; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A;Tille: Complete sequence analysis of the genome of the bacterium Mycoplasma pneu
A;Reference number: S73327; MUID:97105885; PMID:8948633
A;Accession: S73576
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-521 <HIZ>
A;Cross-references: EMBL:AE000025; GB:U00089; NID:g1673918; PIDN:AAB95898.1; PID:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November i
C;Genetics:
A;Genetic code: SGC3
C;Superfamily: hypothetical protein MG068
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c; Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
c; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
c; Accession: AI2436
c; Accession: AI2436
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Accession: AI2436
                                                                                                                                                                                                                                                                                                                                                                                                          A:Cross-references: EMBL:U43738; NID:g1209757; PIDN:AAC43664.1; PID:g1209771 R;Hilbert, H.; Himmelreich, R.; Plagens, H.; Herrmann, R. Nucleic Acids Res. 24, 628-639, 1996 A;Title: Sequence analysis of 56 kb from the genome of the bacterium Mycopla A;Reference number: S62797; MUID:96177562; PMID:8604303 A;Accession: S62798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change
C;Accession: S62794; S62798; S73576
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A;Experimental source: strain PC
C;Genetics:
A;Gene: alr5049
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A; Molecule type: DNA
A; Residues: 1-521 <HIM>
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N;Alternate names: MG395 homolog D02_orf521
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7
                                                                           NID:g1673918; PIDN:AAB95898.1; PID:g16739: to the EMBL Data Library, November 1996
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C.Species: Nus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text
C;Accession: A56940
R;Kasai, K.; Takahashi, S.; Murakami, K.; Nakayama, K.
J. Biol. Chem. 270, 14471-14476, 1995
A;Title: Strain-specific presence of two TGN38 isoforms
A;Reference number: A56940; MUID:95301533; PMID:7540170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Kasai, K.; Takahashi, S.; Murakami, K.; Nakayama, J. Biol. Chem. 270, 14471-14476, 1995. A;Title: Strain-specific presence of two TGN38 isofc A;Reference number: A56940; MUID:95301533; PMID:7540A;Accession: B56940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change
C;Accession: B56940
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C;Species: Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C;Accession: E71729
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
Nature 396, 133-140, 1998
A;Titte: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
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A;Experimental source: strain Madrid E
C;Genetics:
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A; Reference number: A; Accession: A56940
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A; Residues: 1-361 <KAS>
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                                                                                                                                                                                                 RESULT 11
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87.5%;
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88.9%;
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77.88;
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Pred. No.
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                                     mouse
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RESULT 14
JN0453
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A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: E87365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein CC0937 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heat shock proteinase (EC 3.4.21.-) [imported] - Rickettsia conorii (strain Malish C;Species: Rickettsia conorii (C;Date: 30-Sep-2001 *sequence_revision 30-Sep-2001 *text_change 22-Oct-2001 C;Accession: B97729 R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D Science 293, 2093-2098, 2001 A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893 A;Accession: B97729 A;Status: preliminary A;Status: preliminary
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A; Residues: 1-319 <STO>
A; Cross-references: GB:
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Best Local Similarity
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A; Residues: 1-497 <KUR>
                                                                                                                     Query Match
Best Local Similarity 8/...
7; Conservative
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                                                                         222 GNSGGPVF 229
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                                                                                                                                                                                                                                                               GB:AE005673;
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87.5%;
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Pred. No. 31;
0; Mismatches
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Pred. No.
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Pred. No.
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40;
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43;
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C;Accession: AE3453
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dihydroorotate oxidase (EC 1.3.3.1) - gill mushroom (Agrocybe aegerita) N;Alternate names: dihydroorotate dehydrogenase C;Species: Agrocybe aegerita C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-C;Accession: JN0453 R;Noeel, T.; Labarere, J.
Search completed: December Job time: 34.8421 secs
                                                                                    Вр
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                                                                                                                                                                                                                                                         C; Keywords:
                                                                                                                                                                                                                                                                       A; Map position: I
C; Superfamily: dihydroorotate oxidase
                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-364 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52792.1; PID:917983628; GSPDB:GN00190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dihydroorotate oxidase (EC 1.3.3.1) [imported] - Brucella melitensis (strain C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-328 <NOE>
A;Cross-references: GB:M90295; NID:g166337; PIDN:AAA32636.1; PID:g166338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 122, 233-234, 1992
A;TITL1e: Sequence of the URA1 gene encoding dihydroorotate dehydrogenase from the bas
A;Reference number: JN0453; MUID:93083991; PMID:1452035
A;Accession: JN0453
                                                                                                                                                                                                                                                                                                                       A; Gene: BMEI1611
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Best Local Similarity
Matches 7; Conserv
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Pred. No.
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46;
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41;
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                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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13.271 Million cell updates/sec
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                    Published_Applications_AA: *
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: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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US-10-008-355-3
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Sequence 25, Appli
Sequence 4, Appli
Sequence 8, Appli
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Sequence 26, Appli
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Sequence 7, Appli
Sequence 7, Appli
Sequence 9, Appli
Sequence 5, Appli
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Sequence 5, Appli
Sequence 127, Ap
Sequence 1277, A
Sequence 1277, A
Sequence 12, Appli
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Sequence 35385, A
Sequence 2, Appli
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<u>4</u> 5	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20
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US-09-739-861A-5	US-09-795-583-1	US-09-739-861A-1	US-09-853-625B-16	US-09-815-242-13533	US-09-751-798-8	US-10-023-182-8	-0	US-09-864-761-34548	US-09-864-761-35910	US-09-864-761-40613	US-09-735-367B-2	US-09-735-367B-3	US-09-928-457-38	US-09-735-367B-6	US-09-728-910-2	US-09-728-910-4	US-10-052-586-202	US-10-006-867-52	US-10-063-547-52	US-10-066-500-106	-1	US-09-864-761-42729	-09-864-761	US-09-764-869-976	US-09-883-797-8
Sequence 5, Appli		Sequence 1, Appli	Sequence 16, Appl	Sequence 13533, A	Sequence 8, Appli	Sequence 8, Appli	4	Sequence 34548, A	Sequence 35910, A	Sequence 40613, A	2	Sequence 3, Appli	`	6	Ņ	Sequence 4, Appli	Sequence 202, App	Ν	Sequence 52, Appl	Sequence 106, App	Sequence 4, Appli	Sequence 42729, A	34778	ъ.	Sequence 8, Appli

ALIGNMENTS

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; OTHER INFORMATION: Consensus sequence US-10-008-355-25
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US-10-008-355-25
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APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
                                                                                   Sequence 3, Application US/10008355
Patent No. US20020164759A1
GENERAL INFORMATION:
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Patent No. US20020164759A1
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Best Local :
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
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CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 10
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
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FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOETWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 52
TYPE: PRT
ORGANISM: Porphyromonas gingivalis
US-10-008-355-3
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US-10-008-355-8
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: LENGTH: 52
: TYPE: PRT
: ORGANISM: Staphylococcus aureus
US-10-008-355-4
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APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases and Methods Of Use
FILE REFERENCE: 235.00440101
                                SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 699
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/10008355
Patent No. US20020164759A1
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Best Local Similarity
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Best Local Similarity
                                                                                             APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
UNMBER OF SEQ ID NOS: 26
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CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.0
ORGANISM: Porphyromonas gingivalis
                      TYPE: PRT
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                                                                                                                                     ; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Shewanella putrefaciens
US-10-008-355-6
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US-10-008-355-2
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LENGTH: 712
TYPE: PRT
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 10; Conserv
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                                                                                   Query Match
Best Local :
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                                                                     Matches
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APPLICANT: Banbula, Agnieszka
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235,00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
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APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
CURRENT FILING DATE: 2001-11-08
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662 TGGNSGSPVF 671
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                                                                                  Local Similarity
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100.0%; Pred. No. 0.17;
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Pred. No. 1
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Pred. No. 0.17;
                                                                   Mismatches
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US-10-008-355-26

Sequence 26, Application US/10008355 Patent No. US20020164759A1

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Query Match
Best Local Similarity
"atches 9; Conserve
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Best Local Similarity
""" 9; Conserva
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US-10-008-355-9
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TYPE: PRT
; ORGANISM: Xylella fastidiosa
US-10-008-355-7
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                                                                                    GENERAL INFORMATION:
                                                                                                   Sequence 9, Application US/10008355 Patent No. US20020164759A1
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APPLICANT: Banbula, Agnieszka
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEO ID NOS: 26
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
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APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
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647 TGGNSGSPV 655
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%; Pred. No. 1.6
0; Mismatches
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Pred. No.
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APPLICANT: Fellin, Javid R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 09/632,366
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US-09-864-761-48349
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TYPE: PRT
; ORGANISM: Shewanella putrefaciens
US-10-008-355-5
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LENGTH: 720
TYPE: PRT
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Matches 8; Conserv
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PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
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APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
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CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
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APPLICATION NUMBER:

2000-10-04 NUMBER: US 2000-09-27

us 60/236,359

NUMBER: GB 24263.6

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; OTHER INFORMATION: MAP TO AL121716.16
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
; OTHER INFORMATION: EST_HUMAN HIT: BE002805.1, EVALUE 8.00e-39
; OTHER INFORMATION: SWISSPROT HIT: Q9ZKD2, EVALUE 3.60e+00
US-09-864-761-48349
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US-09-815-242-5351
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                   Sequence 5351, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 48349
                   CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                             APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                              APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: 2yskind, Judith W.
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
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Trawick, John D.
Carr, Grant J.
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Xu, H. Howard
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
Type: PRT
COCANIGN. SECTION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 5351
LENGTH: 240
Type: PRT
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
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LENGTH: 254
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Best Local
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APPLICANT: Ohlsen, Ka
APPLICANT: Zyskind,
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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SOFTWARE: FastSEQ for
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                                                                                                                                                            TYPE: PRT
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                                     Similarity 7; Conserv
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Trawick, John D.
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Zyskind, Judith W.
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Sequence 2, Application US/09388089B
Patent No. US20020018782A1
GENERAL INFORMATION:
APPLICANT: Jackson, W.
APPLICANT: Jackson, W.
APPLICANT: HATXIS, A.
TITLE OF INVENTION: NEISSERIA MENINGITIDIS POLYPEPTIDE, NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE AND USES THEREOF
FILE REFERENCE: 7969-083
CURRENT FILING DATE: 1999-08-31
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 447
TYPE: PRT
ORGANISM: Neisseria spp.
                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/388,0898
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 475
TYPE: PRT
RCANISM: Neisseria meningitidis
US-09-388-089B-12
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US-09-388-089B-12
Sequence 12, Application US/09388089B
Patent No. US20020018782A1
Search completed: December 20, 2002, 12:17:26 Job time: 13.6316 secs
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US-09-388-089B-2
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APPLICANT: Jackson, W.
APPLICANT: Harris, W.
APPLICANT: HARRISON: NEISSERIA MENINGITIDIS POLYPEPTIDE, NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE AND USES THEREOF
FILE REFERENCE: 7969-083
                                                                                                                                                      Query Match 66.7%;
Best Local Similarity 75.0%;
Matches 6; Conservative
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Pred. No. 88;
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Pred. No. 82;
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IPR000126; Ser_proteas_V8
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Q9xhh3 lycopersico	P49315 nicotiana p	P29068 thermoactin	Q50336 mycoplasma	Q97pn8 streptococc	032870 mycobacteri	Q50338 mycoplasma	P04459 gallus gall	P45386 haemophilus		P45384 haemophilus	P44969 haemophilus

ALIGNMENTS

STSP_STAAU STAI P04188; 20-MAR-1987 (Rel. (01-APR-1988 (Rel. (15-JUN-2002 (Rel. (20-MAR-1987 (Rel. 04, Created) 01-APR-1988 (Rel. 07, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) Glutamyl endopeptidase precursor (EC 3.4.21.19) (Staphylococcal serine proteinase) (V8 proteinase) (Endoproteinase Glu-C). Rice K., Peralta R., Bast D., de Azavedo J., McGavin M.J.; "Description of staphylococcus serine protease (ssp) operon staphylococcus aureus and nonpolar inactivation of sspA-enco protease."; entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen -!- FUNCTION: PREFERENTIALLY CLEAVES PEPTIDE BONDS ON THE CARBOXYL-TERMINAL SIDE OF ASPARTARE AND GLUTAMATE. -!- CATALYTIC ACTIVITY: Preferential cleavage: Asp-|-Xaa, Glu-|-Xaa-|-SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2B. -!- DATABASE: NAME-Worthington enzyme manual; --- WWW-"http://www.worthington-blochem.com/manual/P/STAP.html". Carmona C., Gray G.L.; "Nucleotide sequence of the serine protease gene of Staphylococcus aureus, strain V8."; Staphylococcus aureus. Bacteria; Firmicutes; EMBL; Y00356; CAA68434.1; -. EMBL; AF309515; AAG45843.1; MEDLINE=78212487; PubMed=96922; SEQUENCE OF 69-280. SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=87316953; PubMed=3306605; nfect. Immun. 69:159-169(2001). SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation primary structure of staphylococcal protease."; J. Biochem. 56:534-544(1978). Res. 15:6757-6757(1987). STANDARD; Bacillales; Staphylococcus PRT; ΑA sspA-encoded serine Glu-|-Xaa in

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Matches 10
                                                                             Svendsen I., Breddam K.;

Svendsen I., Breddam K.;

"Isolation and amino acid sequence of a glutamic acid specific endopeptidase from Bacillus licheniformis.";

Eur. J. Biochem. 204:165-171(1992).

-i. FUNCTION: SPECIFIC FOR HYDROLYSIS OF PEPTIDES BONDS ON THE CARBOXYL SIDE OF ACIDIC AMINO ACID RESIDUES, WITH A STRONG PREFERENCE FOR GLU.

-i. CATALYTIC ACTIVITY: Preferential cleavage: Asp-|-Xaa, Glu-|-Xaa.

-i. SUBCELLULAR LOCATION: Secreted.
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P80057;
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CONFLICT
                                                            This
                                                                                                                                                                                                                                                        Kakudo S., Kikuchi N., Kitadokoro K., Fujiwara T., Nakamura E., Okamoto H., Shin M., Tamaki M., Teraoka H., Tsuzuki H., Yoshida N.; "Purification, characterization, cloning, and expression of a glutamic acid-specific protease from Bacillus licheniformis ATCC 14580.":
   entities
                                                 between
                                                                                                                                                                                                      MEDLINE-92155199;
                                                                                                                                                                                                                   SEQUENCE OF 95-316.
                                                                                                                                                                                                                                                                                                             STRAIN-ATCC 14580;
MEDLINE-93054737; PubMed-1429718;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND
                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; NCBI_TaxID=1402;
                                                                                                                                                                                                                                                                                                                                                                                  Bacillus licheniformis.
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01-OCT-1993
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PROSITE; PS00672; V8_HIS; 1.
PROSITE; PS00673; V8_SER; 1.
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           ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in filed and this statement is not removed. Usage by and for con
                                                SWISS-PROT entry is copyright. It is produced through a collaboration -
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10; Conserv
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D -> N (IN REF. 3).
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ENV -> NEVN (IN REF. 3).
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Pred. No. 0.027;
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(EC 3.4.21.19)
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noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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            is in no way for commercial
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(ESULT 3)

ER24_HUMAN STANDARD;
ID ER74_HUMAN STANDARD;
AC 076062; 095982; 096c21; 096c64;
AC 076062; 095982; 096c21; 096c64;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Delta(14)-sterol reductase (EC 1.3.1.70) (C-14 sterol reductase)
C14-reductase) (Delta14-SR) (Transmembrane 7 superfamily sterol c14-reductase) (Putative sterol reductase SR-1).
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InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
PRINTS; PR00039; Tryp_Sin; 1.
PROSITE; PS00672; V8_HIS; 1.
PROSITE; PS00673; V8_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                Strausberg R.;
Submitted (MAY-2001) to
                                                                                                                                                                                                  MEDLINE=98277456; PubMed=9615229;
Lemmens I.H., Kas K., Merregaert J., Van De Ver
"Identification and molecular characterization
gene cluster on human chromosome 11q13.";
Genomics 49:437-442(1998).
                               Roberti R.,
Beccari T.,
                                                                                                                                     Genomics 54:469-476(1998).
                                                                                                                                                                   SEQUENCE FROM N.A., SUBCELLULAR L
MEDLINE=99097347; PubMed=9878250;
                                                    PubMed=11784322;
                                                              FUNCTION
                                                                                                      TISSUE=Brain, and
                                                                                                                SEQUENCE FROM N.A
                                                                                                                                               "The human lamin B receptor/sterol reductase
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         liver
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A45134; A45134.
Biochem.
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                  , Bennati A.M.,
, Della Fazia M.
nd expression of
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269:283-290(2002)
                                                                                                     Eye;
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of sterol Deltal4-reductase
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CHARGE RELAY SYSTEM (B)
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EMBL; AF096304; AAD09765.1; --
EMBL; BC009052; AAH09052.1; --
EMBL; BC012857; AAH12857.1; --
EMBL; BC012857; AAH12857.1; --
EMBL; BC012857; AAH12857.1; --
EMBL; BC012857; AAH12857.1; --
SEQUENCE FROM N.A. STRAIN-ATCC 29342 MEDLINE-96177562;
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                                                                                    MPN592
                                                                                            Hypothetical lipoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                               NCBI_TaxID=2104;
                                                             Bacteria;
                                                                       Mycoplasma
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001171; ERG4_ERG24.
                                                                                                                                 16-OCT-2001
                                                                                                                                                                                                                   163 GGNSGNPIY 171
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CATALYTIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   but not detected in placenta, spleen, thymus, small intestine, colon (mucosal lining), or peripheral blood leukocytes.
SIMILARITY: BELONGS TO THE ERG4/ERG24 FAMILY.
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beta-ol + NADPH
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                                                          Firmicutes;
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13 35
62 124
102 124
129 148
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                                                                                                        (Rel. 40, Created)
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                                                          Mycoplasmataceae; Mycoplasma
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PYRD_AGRAE
ID PYRD_AAA
AC P28294
DT 01-DEC
DT 15-JUN
DE Dihydr
DE (DHOde
GN URAL)
OS Agrocy
OC Agaric
OX NCBLT
RN [1]
RP SEQUEN
RX MEDLIN
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RL Gene 1
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Best Local
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                                                                                                                                                                                                                                 PYRD_AGRAE STANDARD; PRT; 328 AA.
P28294;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Dihydroorotate dehydrogenase (EC 1.3.3.1) (Dihydroorotate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a clear the Ewiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence analysis of 56 kb from the genome of the bacterium Mycoplasma pneumoniae comprising the dnaA region, the atp operon cluster of ribosomal protein genes.";
Nucleic Acids Res. 24:628-639(1996).
H(2)O(2).
-!- COFACTOR: FAD.
-!- PATHWAY: Pyrimidine biosynthesis; fourth step.
                                             "Sequence of the URA1 gene encoding the basidiomycete fungus Agrocybe ac Gene 122:233-234(1992)
-i- CATALYTIC ACTIVITY: (S)-dihydroc
                                                                                                                                                                    Eukaryota; Fungi; Basidion Agaricales; Bolbitiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01727; DUF30; 1. Pfam; PF01732; DUF31; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U43738; AAC43664.1; -. EMBL; AE000025; AAB95898.1; -.
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STRAIN=ATCC 29342 / M129;
                                                                                                              SEQUENCE FROM N.A.
MEDLINE=93083991; PubMed=1452035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00840; Y06768FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002414; DUF30/31. Pfam; PF01727; DUF30; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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                                                                                                    Noel T., Labarere J
                                                                                                                                                                                                 Agrocybe aegerita
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae."
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                                                                                                                                                                                                                          (DHOdehase)
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                                                                                                                                                                 Basidiomycota; Hy
tiaceae; Agrocybe.
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77.8%;
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                                              (S)-dihydroorotate
                                                                        Agrocybe aegerita
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N-ACYL DIGLYCERIDE (POTENTIAL).
; 0E706CDEC8CEEBDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
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                                                                                                                                                                                  Hymenomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 521;
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                                                                                                                                                                                  Homobasidiomycetes;
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Best Local S
Matches 7
InterPro; IPR00202; Amb_allergen.
Pfam; PF00544; pec_lyase; 1.
Lyase; Signal; Glycoprotein; Multi(
SIGNAL 1 20 OR 21
CHAIN 21 378 PECTTO
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15-JUL-1998
15-DEC-1998
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pIR; JN0453; JN0453.
InterPro; IPR001295; DHO_dh.
pfam; PF01180; DHOdehase; 1.
TIGREAMS; TIGR01036; PYTD_sub2; 1.
                                                                              EMBL;
HSSP;
                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See )
                                                                                                                                                                                                                                                                                                                                    Kusters-Van Someren M., Flipphi M., de Graaff L., Kester H., Hinnen A., Visser J.; Kester H. Hinnen A., Visser J.; "Characterization of the Aspergillus niger pelB ge regulation of expression."; Mol. Gen. Genet. 234:113-120(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00911; DHODEHASE_1; 1.

PROSITE; PS00912; DHODEHASE_2; 1.

PyrImidine biosynthesis; Oxidoreductase; Flavoprotein; FAD.

NP_BIND 288 296 FAD (NAD PART) (POTENTIAL).

SEQUENCE 328 AA; 35085 MW; 71FA3D2A4D57EF75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus niger.
Eukaryota; Fungi;
Eurotiales; Tricho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-92357005; PubMed-1495474;
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                                                                                                            EMBL; X65552;
                                                                                                                                            or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5061;
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SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Eliminative cleavage
                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Eliminative cleavage of pectin to give oligosaccharides with terminal 4-deoxy-6-methyl-alpha-D-galact-4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Cytoplasmic (Probable).
                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collab een the Swiss Institute of Bioinformatics and the EMBL outset European Bloinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in fied and this statement is not removed. Usage by and for compared the statement is not removed.
                                                                       X65552; CAA46521.1; -. A12248; CAA01023.1; -. Q01172; IIDJ.
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                                                                                                                                            an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trichocomaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 37, Last annotation update)
B precursor (EC 4.2.2.10) (PLB).
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               Multigene family OR 21 (POTENTIAL)
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                (POTENTIAL)
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Matches 7
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Best Local
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P09506;
01-MAR-1989 (Rel. 1
01-MAR-1989 (Rel. 1
01-OCT-1989 (Rel. 3
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CARBOHYD
CARBOHYD
SEQUENCE
                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 44, Last annotation update)
Hypothetical 110.9 kDa protein in SPC98-TOM70
YNL123W OR N1897.
                                                                                                           YNM3_YEAST
P53920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _BWYVF
                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                 InterPro; IPR000382; Luteo_ORF2;
Pfam; PF02122; Luteo_ORF2; 1.
PRINTS; PR00913; LVIRUSORF2.
                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=89057523; PubMed=3194229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beet western yellows virus (isolate FL-1) (BWYV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.2 kDa protein (ORF 2).
NCBI_TaxID=4932;
           Saccharomycetales;
                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Veidt I., Lot H., Leiser M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=12043;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of beet western yellows virus RNA."; 
Nucleic Acids Res. 16:9917-9932(1988).
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378
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(Rel. 10, Last seq
(Rel. 12, Last ann
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                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TO POTATO LEAFROLL VIRUS ORF2.
           Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255
128
251
39703
                                                                                                                                                                                                                                                                                     66210 MW;
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77.8%;
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Last annotation update)
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Pred. No.
                                                                                                                                                                                                                                                 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scheidecker D.,
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N-LINKED (GLCNAC. . .) (POTENTIAL)
; 4FF321AF2B0B72FF CRC64;
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                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                     2A41F82911DEC84F CRC64;
                                                                                                                                                                                                                                       Mismatches
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            Saccharomyces
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                                                           intergenic
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                            RRPO_BWYVF
P09507;
                                                                                                                                                                        REVISIONS.
Veidt I., !
                                                                                                                                                                                                                                                                                                                                                 01-MAR-1989 (kel. 10, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative RNA-directed RNA polymerase (EC 2.7.7.48) (ORF 3).
Beet western yellows virus (isolate FL-1) (BWYV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical SEQUENCE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001478; PDZ.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00595; PDZ; 1.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae reveals an unusually high number of overlapping open reading frames."; Yeast 13:261-266(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  de Antoni A., D'Angelo M., Dal Pero F., Sartorello F., Pal
Pallavicini A., Lanfranchi G., Valle G.;
"The DNA sequence of cosmid 14-13b from chromosome XIV of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                             Submitted (APR-2002) to -!- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 269382;
EMBL; 271399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97245296; PubMed=9090055;
                                                                                                                                                                                                    Nucleic Acids [2]
                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                          Veidt I., Lot H.,
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-89057523;
                                                                                                                                                           Jonard G.;
                                                                                                                                                                                                               Nucleotide sequence of beet western yellows Nucleic Acids Res. 16:9917-9932(1988).
                                                                                                                                                                                                                                              Jonard G
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=12043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TGGNSGSPV
                                                                                                     SIMILARITY: 70% SIMILARITY TO POTATO LEAFROLL VIRUS ORF3
                                                                          AND PARTIAL SIMILARITY TO SOU RNA-DEPENDENT RNA POLYMERASE.
                                                                                                                     (RNA)(N).
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                                                                                                                                                                        Lot H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l protein
997 AA;
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                                                                                                                                                                                                                                                                        PubMed=3194229;
                                                                                                                                                                                                                                                        Leiser M.,
                                                                                                                                                                          Leiser
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77.8%;
                                                                                                                              the EMBL/GenBank/DDBJ databases
N nucleoside triphosphate = N di
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Pred. No. 36;
2; Mismatches
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                                                                                                                                                                     Scheidecker D.,
                                                                                                                                                                                                                                                        Scheidecker D.,
                                                                                       SOUTHERN BEAN MOSAIC VIRUS PUTATIVE
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There are no restong as its content
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                                                                                                                                                                     Guilley H.,
                                                                                                                                                                                                                              virus RNA.";
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RESULT 10
PYRD_ARATH
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Best Local
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                             NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                  EMBL; X62909; CAA44695.1; -.
PIR; S23702; S23762.
InterPro; IPR001295; DHO_dh.
InterPro; IPR003009; FMN_enzyme.
                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=93272056; PubMed=1303803;
Minet M., Dufour M.E., Lacroute F.;
"Complementation of Saccharomyces cerevisiae auxotrophic mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Dihydroorotate dehydrogenase, mitochondrial precursor (EC 1.3.3.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X13063; CAA31464.2; -.
PIR; S01940; RRVQFL.
InterPro; IPR001795; Luteo_RNA_pol.
                                                                                              TIGREAMS; TIGRO1036; pyrD_sub2; 1.
PROSITE; PS00911; DHODEHASE_1; 1.
PROSITE; PS00912; DHODEHASE_2; 1.
Pyrimidine biosynthesis; Oxidoreductase; Flavoprotein; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana cDNAs.";
Plant J. 2:417-422(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02123; Luteo_ORF3; 1. PRINTS; PR00914; LVIRUSRNAPOL.
                                                        CHAIN
                                                                     Transit peptide; Mitochondrion.
TRANSIT 1 ? MI
                                                                                                                                                      Pfam; PF01180; DHOdehase; 1.
                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: Pyrimidine biosynthesis; fourth step.
                                                                                                                                                                                                                                                                                                                                                                                -! - COFACTOR: FAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; RNA-directed RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Dihydroorotate oxidase) (DHOdehase).
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                             393
434
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                              ΑĀ;
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                           45568 MW;
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77.8%;
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  70.48;
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                                          FAD
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 Score 38;
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                                                                    MITOCHONDRION (POTENTIAL)
                                                       DIHYDROOROTATE DEHYDROGENASE
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                             186BA05F3EF49D91 CRC64;
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                                            PART)
 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Embryophyta; Tracheophyta;
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Length 434
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HME1_MOUSE
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                              EMBL; L12703; AAA03660.2; -.
EMBL; Y00201: CAA68361.1; -.
PIR; A26629; A26629.
PIR; A24778; A24778.
PIR; A24778; A24778.
PIR; S13009; S13009.
PIR; A48423; A48423.
PIR; A48423; A48423.
                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                           homology to the Drosophila Cell 43:29-37(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE-93185339, PubMed=1363401;

Logan C., Hanks M.C., Noble-Topham S., Nallainathan D.,

Provart N.J., Joyner A.L.;

"Cloning and sequence comparison of the mouse, human, and chicken
"cloning and sequence potential functional domains and regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Last sequence upd 15-JUN-2002 (Rel. 41, Last annotation u Homeobox protein engrailed-1 (Mo-En-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HME1
                                                                                                                                                                                                                                                                                                                                Joyner A.L., Kornberg T., Coleman K.G., Cox 
"Expression during embryogenesis of a mouse 
homology to the Drosophila engrailed gene."
                                                                                                                                                                                                                                                                                                                                                                                                  Joyner A.L., Martin G.R.;
Joyner A.L., Martin G.R.;
"En-1 and En-2, two mouse genes with sequence homology to the "En-1 and En-2, two mouse genes with sequence homology to the
                                                                                                                    entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                     evolution.
                                                                                                                                                                                                                                                             Holland P.W.H., Williams N.A.; "Conservation of engrailed-like homeobox sequences
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 298-401 FROM N.A. MEDLINE=86079501; PubMed=2416459;
                                                                                                                                                                                                                                                                                                                                                                                                Drosophila engrailed gene: expression Genes Dev. 1:29-38(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                     MEDLINE=91099509; PubMed=1980115;
                                                                                                                                                                                                                                                                                                SEQUENCE OF 321-380 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88112776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF
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                        CRANSFAC;
                                                                                                                                                                                                                                           FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus (Mouse)
                                                                                                                                                                                                          SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE ENGRAILED HOMEOBOX FAMILY.
SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
          SFAC; T02016;
MGI:95389; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _MOUSE
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                                                                                                                                requires a license agreement (See http://www.isb-sib.ch/announce/
IPR000747;
                                                                                                                                                                                                                                          277:250-252(1990).
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Engrailed
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annotation update)
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                                                                                                                                                                                                                                                                                                                                          sequence
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                             [nterPro;
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RESULT 12
CEL1_AGAB
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Matches 6
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Q00023;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS00033; ENGRAILED; 1.
                                                                                                                                                                                                                                                                                                                                       Armssilla A.L., Thurston C.F., Yaguee E.;
"CELL: a novel cellulose binding protein secreted by Agaricus bisporus during growth on crystalline cellulose.";
FEMS Microbiol Lett. 116:293-299(1994).
-i- FUNCTION: PROBABLE GLYCOSYL HYDROLASE ACTIVE ON CELLULOSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agaricus bisporus (Common
Eukaryota; Fungi; Basidio
Agaricales; Agaricaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homeobox; DNA-binding; Developmental promain 52 87 PRO-RICH DOMAIN 73 87 POLY-PRO-
                                               EMBL; M86356; AAA53434.1; HSSP; P00725; 2CBH.
                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
-!- SIMILARITY: BELONGS TO FAMILY 61 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-D649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cellulose-growth-specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94237428; PubMed=8181702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5341;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Raguz S., Yaguee E., Wood D.A., Thurston C.F.;
"Isolation and characterization of a cellulose-growth-specific gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00046;
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                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agaricus bisporus.";
119:183-190(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conserv
IPR000254; CBD_fungal.
IPR005103; Glyco_hydro_61.
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Basidiomycota; Hy
caceae; Agaricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=1398098;
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75.0%;
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POLY-ALA.
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1F90210950152FAE CRC64
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PF00734; CBM_1; 1. PF03443; Glyco_hydro_61; 1.

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RESULT 13
PLYA_COLGL
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DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                    MEDLINE=94237480; PubMed=8181749; Pemnleton M.D., Sharrock K.R., Bo
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15-DEC-1998
15-DEC-1998
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DOMAIN
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CHAIN
                                           SEQUENCE
                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                          Pfam; PF00544; pec_lyase; 1.
Lyase; Signal; Glycoprotein.
SIGNAL 1 20
                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                   "The pectin lyase-encoding gene (pnl cingulata: characterization of pnlA Gene 142:141-146(1994).
-!- CATALYTIC ACTIVITY: Eliminative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLYA_COLGL
Q00374;
                                                                                                                      EMBL; L22857; AAA21817.1; HSSP; Q01172; 1IDJ.
                                                                                                                                                                                                                                                                                                                                 Templeton M.D., Rikkerink E.H.;
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota;
Sordariomycetes incertae sedi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                         InterPro; IPR002022; Amb_allergen
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                                                                                                                                                                                                                                                                                                                                                                                                                                 cingulata).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pectin lyase
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 Similarity 6; Conserv
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262
286
292
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163
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380
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(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update)
precursor (EC 4.2.2.10).
 Conservative
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POTENTIAL.
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BY SIMILARITY.
N-LINKED (GLCN)
Score 36; DB Pred. No. 43; 2; Mismatches
 2;
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Pred. No.
                                          N-LINKED (GLCNAC. . .) (POTENTIAL);
3DF9A99FBB482053 CRC64;
                                                                PECTIN LYASE
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CELLULOSE-BINDING
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                                                                            POTENTIAL
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s; Phyllachorales; Phyllachoraceae;
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                                                                                                                                                                                                                                                                                                                                          Bowen J.K., Crowhurst R.N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -LINKED (GLCNAC. . 60E2C8080895CA2B
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4-deoxy-6-methyl-alpha-D-galact-4-
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36;
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                    Length 380;
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MBL outstation -
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RESULT 14
Y350_HAEIN
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  Query Match
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01-MAR-1992
01-NOV-1995
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=RM 7004 / Serotype B;
MEDLINE-92065797; PubMed-1956282;
Maskell D.J., Szabo M.J., Butler P.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical HI0350.
                                                                                                                                                                                                                            Hypothetical Complete pro
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Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y350_HAEIN
                                                                                   SEQUENCE
                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                           TIGR; HI0350;
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U32719; AAC22011.1;
  Similarity 7; Conserv
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TIGR00901; 2A0125; 1.
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(Rel. 32, Last sequence up
(Rel. 41, Last annotation
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Matches 6
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InterPro; IPR001478; PDZ.
InterPro; IPR001254; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00595; PDZ; 2.
PRINTS; PR00834; PROTEASES2C.
SMARF; SM00228; PDZ; 2.
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SIGNAL
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
DEGP OR HTRA OR RC0166.
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-i- SIMILARITY: BELLONGS TO PEPTIDASE FAMILY S2C.
-i- SIMILARITY: CONTAINS 2 PDZ/DHR DOMAINS.
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Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID-781;
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CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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E03836.1 GI:2172050
JP 1992211370-A/2
Staphylococcus aureus
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S. aureus glutamic acid specific protease (EC 3.4. D00730 D00730.1 GI:216970

V8-like protease; glutamic acid specific protease. S. aureus (strain ATCC12600) genomic DNA. Staphylococcus aureus
                                                                                                                    E03836

DNA encoding V8 protease.
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Fax:
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Purification, characterization and gene cloning of a novel glutamic acid-specific endopeptidase from Staphylococcus aureus ATCC 12600 Blochim. Biophys. Acta 1121 (1-2), 221-228 (1992)
Staphylococcus aureus
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1 (bases 1 to 1289)
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/note="(ProAsxAsn) sequence"
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DKQQTPKIQKGCNLKPLEQCREANVILPNNDRHQITDTTNGHYA,PVTYIQVEAPTGTF
IASGVVVGKDTLLTNKHVVDATHGDPHALKAFVSAINQDNYPNGGFTAPQITKYSEGE
DLAIVKFSPNEDNKHICEVVKPATMSNNAETQVVQNITYTGYPGDKPVARMESKGKI
TYLKGEAMQYDLSTTGGNSGSPVFNEKNEVIGIHWGGVPNQFNGAVFINENVRHFLKQ
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/transi_table=11
/product="glutamic acid specific protease prepropeptide"
/protein_id="pax00630.1"
/db_xref="GI:216971"
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/db_xref="taxon:1280"
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US-10-008-355-26 (1-9)
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Best Local Similarity:
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SHIONOGI & CO LTD
OS Stabhylococcus
PN JF 1992211370-
PD 03-AUG-1992
PF 19-EB-1991 JF
PR 20-FEB-1990 JF
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OS Staphylococcus
PN JP 1992211370
PD 03-AUG-1992
PF 19-FEB-1991 JF
PR 20-FEB-1990 JF
PI NAKAMURA ETSUC
                                                                                                                           JP 199211370-A/1.
Staphylococcus aureus.
Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
1 (bases 1 to 1886)
Nakamura, E., Tamaki, M., Teraoka, H., Matsumoto, K., Fujiwara, K., Tsuzuki, H., Yoshida, N. and Kakudou, Standard Research
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                                Staphylococcus aureus
JP 1992211370-A/1
03-AUG-1992
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Feature is identified by similarity;
Key Location/Qualifiers
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hypothetical: No;
anti-sense: No;
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JP 1992211370-A/2
 19-FEB-1991 JP 1991024633
20-FEB-1990 JP 90P 4031
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20-FEB-1990 JP 90P 403
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40398

/db_xref="GI:46687"

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REFERENCE
AUTHORS
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                             SASP
Staphylococcus aureus V8
Y00356
                                                                                                                                                                                                                                                                    Staphylococcus aureus Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                          serine protease.
Staphylococcus aureus.
                                                                                                                                        Nucleic Acids Res. 15 (16),
87316953
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C12N9/52,C12N15/57,(C12N15/57,C12R1:445);
strandedness: Double;
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*source: clone=pAM82SIGV8;
Feature is identified by experimental;
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/db_xref="taxon:1280"
302 c 219 g 476 t
/protein_id="CAA68434.1"
                               /note="preproenzyme (AA
                                              354. .1364
                                                      /db_xref="taxon:1280"
/clone="pV8CO"
                                                                               /organism="Staphylococcus
/strain="V8"
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                     /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 3240)
Rice, K.C. and McGavin, M.J.
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Infect. Immun. 69 (1), 159-169 (2001)
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/translation="MKGKFLKVSSLFVATLITATLVSSDAANALSSKAMDNHPQQTQS
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DLAIVKFSPNEQNKHIGEVVKPATMSNNAETQVNQNITVTGYPGDKPVATMWESKGKI
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1218. 1325
/note="twelvefold repeated tripeptide (Pro-Asp-Asn)"
1 296 c 231 g 490 t
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354. .557
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NIEDIHFANDDQPNNPDNPNNPDNPNNPDNPNNPDEPNNPDNPDNPDNPDNSDNNNSDNPD
                                                                                        endopeptidase"
                                                                                                                                           /gene="sspA"
354. .1364
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354. .1364
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/note="serine
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/db_xref="taxon:1280"
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Cysteine proteinase; glutamyl endopeptidase; msrwl
proD gene; proM gene; spwl gene.
                                                                                      and msrwl gene.
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EDQVQYENTLKNFKIREQQFDNSWCAGFSMAALLNATKNTDTYNAHDIMRTLYPEVSE
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DLAIVKFSPNEQNKHIGEVVKPATMSNNAETQVNQNITVTGYPGDKPVATMWESKGKI
TYLKGEAMQYDLSTTGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQ
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SKQQTPKIQKGGNLKPLEQREHANVILPNNDRHQITDTINGHYAPVTYIQVEAPTGTF
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1554. .2624
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Genetic and biochemical characterization of glutamyl endopeptidase of Staphylococcus warneri M
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DB:
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                                                                                      AUTHORS
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2 (bases 1 to 10689)
Simpson, A.J.G., Reinach, F.C., Arruda, P., Abreu, F.A., Acencio, M., Alveson, A.J.G., Relach, F.C., Araya, J.E., Bala, G.S., Baptista, C.S., Barros, M.H., Bonaccorsi, E.D., Bordin, S., Bove, J.M., Briones, M.R.S. Bueno, M.R.P., Camargo, A.A., Camargo, L.E.A., Carraro, D.M.,
                                                                                                                                                                                                                                       The genome sequence of the plant Xylella fastidiosa Consortium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xylella fastidiosa 9a5c.
Xylella fastidiosa 9a5c
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                                                                                                                                                                                       Sequencing and Analysis
Nature 406 (6792), 151-157 (2000)
                                                                                                                                                                                                                                                                                             and Marino, C.L.
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                                                                                                                                      10910347
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Costa~Neto,C.M., Coutinho,L.L., Cristofani,M., Dias~Neto,E.,
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                                                                                                       gene
                                                                                                                                                                          /translation="MCSRSFFLYFISALGLTLVISFPECLFAQNVPPTVEVVPTSVRY
SSVISDGVSTSATFEARSTALVNGVRYYTVPVDISASTLGSLAKVAVBRGMAFYNVYS
MLSGLINGAGWVIDELTHEVMSGPALKEIPVGTVAMWQRPGDGHVFYSVTPQGLIAP
INAYQSSLSPPOPLYMSSGPSSVSSERWLYHLEGGGEYIGHLSKTDQSVPDYSSGLPP
SVILDTDLGQLVRSDPSTVNAVLTDSQTGAVLLTPEIVSALNKLRRSLEDELKASHAP
DQQPSSGGASSPPSSSGTAWPSFCSWASVVCDFIDWVKSDEFLKKFLVPPDVPYYDKL
                                                     complement(4481. .4702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="hypothetical protein; identified by sequence
similarity; putative; ORF located using Glimmer/RBSfinder"
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complement(3195. .4412)
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complement(2918. .3202)
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DTHRHGGYDLMFVTQWPTKIHHELRRLVGEHVHLNRAMGLQTAGLYRWSRAQDDPYDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to SP|P03626 (percent identity: 36 %/query alignment coverage: 88.0 %/subject alignment coverage: 105.0 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"hypothetical protein"
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..."
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/gene="XF1875"
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similarity; putative; ORF located using Glimmer/RBSfinder"
/note="hypothetical protein; identified by sequence
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                                                                             /gene="XF1878"
                                                                                                     complement(4481. .4702)
                                                                                                                                  AYIAGGFRGVKNV"
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YYSPAHLSEAASSVAGASGQASLRAAPASLSSSRSLYSGMRTYAVLETESAPTLSGCV
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1351. .1662
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AP004825/c
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US-10-008-355-26 (1-9)
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AP004825 290150 bp DNA linear BCT 02-JU Staphylococcus aureus subsp. aureus MW2 DNA, complete genome, strain: MW2, section 4/10.
AP004825 BA000033
AP004825.1 GI:21203989
                                                                                                                                                                                                                                                                                        Aoki,K., Oguchi,A., Nagai,Y., Asano,K., Iwama,N., Baba,T., Kuroda,M., Hiramatsu,K. and Kikuchi,H.
Direct Submission
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         community-acquired MRSA
Lancet 359 (9320), 1819-1827 (2002)
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Genome and virulence determinants of high virulence
                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 290150)
/organism="Staphylococcus
/strain="MW2"
/db_xref="taxon:196620"
285. .1493
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similarity; putative; ORF located using Glimmer/RBSfinder"
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PHIVMCFLVAWGFHFLFTVVRD"
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                                                                             aureus
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IELDFHEGISIGQSINLARDFSNMPPNVLTPQTFAEDIVNHFKNTKVKVDVKDYDTL
VSEGFGLLQAVGKGSKHKPRLVTITYNGKDKDEAPIALVGKGITYDSGGYSIKTKNGM
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4845. .5219
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WYELDAKFVEGIKIMAYIGVVILTANGFAGVMNATGDIDELVKTLTSITGDNKLFSII
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TINFGRNIVDGAEVALSYALLGGFAALLSYSGITDVLVGKIIANIAEMSRWSRWSVKVV
VTIILALLAMSIMSQNLIGTPAHIAFIBTVIPFLLSTBRUKIDRRLIGHGLGFV
VTILALGARINGORIGHSTBRUKINSTRIKATORIKANIA SARANIA 
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3510. .4826
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VEVMNTDAEGRLVLADAVFYANQYQPSVIMDFATLTGAAIVALGDDKAAAFESNSKVI
LNDILQISSEVDEMVEELPITATERASIKHSDIADLVNHTNGQGKALFAASFVTHFSG
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1624. .3099
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                                                                                                                                      complement(5275. .6429)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="MW0826"
/note="ORFID:MW0826"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDSTLGPTAGLNVDGQHDHIRDTCVPNFLFYNIPLMIFGTIAAMVL"
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/protein_id="BAB94689.1"
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                                                                                               /gene="MW0827"
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                                                    /note="ORFID:MW0827"
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                                      complement(9275. .9616)
/gene="mnhC"
/note="ORFID:MW0832"
                                                                                                                                 /gene="mnhC'
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QNVNHIFEKEHDQVYYDKTDHIVGSGITAAHLALKLLNHDNDKKIHLMLNKDIEIHDF
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STLGAMSLLFGTFLYFIATQGFVNMQLIVAIIFVLITGPLSSHMIMKAAYNIKTPYTK
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complement(9275.
                                FYGKFFIVQSTFERGFYLSGVIVLLSSLVVLYSVIRIFLQGFFGQPKGYDLNNKVDVK
YLTTIAIVAVVITVLYGLSADYLYPMVKAGAETFYNPSTYVKAVLGGK"
                                                                                                                                                                                                                                                                                                                                           /product="Na+/H+-antiporter subunit"
/protein_id="BAB94696.1"
/db_xref="GI:21203998"
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/gene="mnhE"
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/gene="mnhE"
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/protein_id="BAB94694.1"
/db_xref="GI:21203996"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(7012. .7305)
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/gene="mnhf"
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TPITQISDGLINTENNSVPYQQIMVATGFEQDFMSQPLIKQLIQNYDAPINECNYPVI
                                                                                                                                     YVILFLALLTIIFGCVGAVAYANIKKIILYNVMIAVGVILVGVAMMTESGMIGAIYYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="Na+/H+ antiporter subunit"
/protein_id="BAB94695.1"
/db_xref="GI:21203997"
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/db_xref="GI:21203995"
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                                                                                                    JHDMLVKLALFLLIGIMIKITGTADLRQFGGLIKRYPVLGWSFFIAALSLAGIPPLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="ORFID:MW0831"
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                                                 Submitted (30-JAN-2001) Akio Oguchi, National Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:oguchi@nite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-8424)
On Jun 12, 2001 this sequence version replaced gi:13700734.
                                                                                                                                                                                                                                                         2 (bases 1 to 298050)
Aoki, K., Oguchi, A., Hosoyama, A., Nagai, Y., Kuroda, M., Hiramatsu, K. and Kikuchi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus subsp. aureus N315 (sub_species:aureus N315, strain:N315) DAA.
Staphylococcus aureus subsp. aureus N315
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome, section 4/10.
AP003132 BA000018
AP003132.2 GI:14349174
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                                                                                                                                                                                                                                  Direct Submission
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21311952
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VESMKGVPEDD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [PLFILEPVHMTTAVFFDFGVLCAVVGTVMTIIISIGENE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="murqqudLILqFAAVIIFFMVMVFGFSLFLAGHYTPGGGFVGGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Na+/H+ antiporter subunit"
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Indels:
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Matches:
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3134. .3370
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/note="ORFID:SA0795"
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1902. 3116
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WKLIQFISFPTISSGPIDRYKRFVKDDKKVPTGNEYRELVLKAIHMIMLGFLYKYIV
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448. .1905
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FDKPFKAKNIKDFWNRWHMTLSFWFRDCIYMRSLFYMSRKKLLKSQFAMSNVAFLINF
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/transl_table=11
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YEFNVNSPEFQDLELLVKTMRAAGADVQYVSIPSNGVWYDHIGIDKERRQAVYKKIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRLASILKSGVLWLYKYHNG<sup>®</sup> 6911. .7147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESRSDLEIYLYDRGPRILRNFPEKLSKYVAKWFAKNNVTVVPNSNINKVEPGKIYNCD
EPKDIDLVVWTAGIQPVEVVRNLPIDINSNGRVIVNQYHQVPTYRNVYVVGDCADLPH
APSAQLAEVQGDQIADVLKKQWLNEPLPDKMPELKVQGIVGSLGDKQGFAYIMDRTVT
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                                                                                                                                              /gene="SA0801"
7160. .7519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="ORFID:SA0797
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MEDLINE
REFERENCE
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VERSION
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                                                                                                                                                                                                                                                                                       TITLE
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                                                                                                                                                                                                                                                                                                                                         AUTHORS
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Db 123979 ACTGGTGGTAACTCAGGTTCACCTGTA 123953
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                                                                                                                                                                                Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College of Medical Technology and Nursing, Department of Medical Technology; 1-1-1 Ten-noodai, Tsukuba, Ibaraki 305-8577, Japan (E-mail:tohta@sakura.cc.tsukuba.ac.jp, Tel:81-298-53-3454, Fax:81-298-53-3454)
On May 29, 2001 this sequence version replaced qi:13875305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus subsp. aureus sequence, section 4/9.
AP003361 BA000017
AP003361.2 GI:14246761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I., Cui, L., Oguchi, A., Aoki, K., Nagai, Y., Lian, J., Ito, T., Kanamori, M., Matsumaru, H., Maruyama, A., Murakami, H., Hosoyama, A., Mizutani-Ui, Y., Takahashi, N.K., Sawano, T., Inoue, R., Kaito, C., Sekimizu, K., Hirakawa, H., Kuhara, S., Goto, S., Yabuzaki, J., Kanehisa, M., Yamashita, A., Oshima, K., Furuya, K., Yoshino, C., Shiba, T., Hattori, M., Ogasawara, N., Hayashi, H., and Hiramatsu, K.
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Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillales; Staphy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Whole genome sequencing of meticillin-resistant Staphylococcus
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35. .1021
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                                                                                                                                                          location/Qualifiers
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AMSLIITYIISFALGIISGRYSYSLTDYTVQIIRVIMLAIPSE AGVIAIFIESEELQ
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2971. .3852
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1024. .2004
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VLSWGGIARLVRGKVLQEKENEYFLAAKSIGTPTYKIILKHLLPNILSVVIVQATLLF
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/gene="SAV1000"
/codon_start=1
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MGEEYLNVVKEGLNNWWDDYENKGKRSGGYSSGAHLTNPFILLMWSNTISDLYTLVH
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ITMPODRIKLERQTRQLAAIYLASGIDPDKATLEIQSEVPAHYQAGWMLTTIASVGEL
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SKEWSRIPHFYMNYYVYQYATGYSAAQSLSHQILTEGKPAVDRYINEFLKKGSSNYPI
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6783. .7769
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NPITTEFEDLLYMVDGTYYYAVHFDSHVDQEVINDSYSOLLEFAYPTDRTEVYLNDYA
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VGYNEDEIRRFLPRKVRTFQLQEAQRMVD"
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5177. .5572
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Submitted (16-JUN-
Chicago, 840 S. Wo
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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840 S. Wood St. (M/C 787),
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MEDLINE
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Homo sapiens BAC clone RP11-9D8
AC108022 AC009566
AC108022.3 GI:19339101
                                                                                                                                                                                                                                                                     Direct Submission Submitted (11-MAR-2002) Genome Sequencing Center, Washington Submitted (21-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                             Submitted (20-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Mar 11, 2002 this sequence version replaced gi:18693535.
                                                                                                                                                                                                                                                                                                                                                               MO 63108, USA
5 (bases 1 to 162609)
                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-FEB-2002) Genome University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (24-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 (bases 1 to 162609) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cedroni, M., Kozlowicz, A. and
The sequence of Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998) 99063792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 162609)
Sulston, J. E. and Waterston, R.
                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                               Waterston, R.
                                                                                                                                                                                                                                                                                                                                               Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 162609)
Center project name: H_NH0009D08
Drafting Center: WIBR
                                                      Web site: http://genome.wustl.edu/gscContact: sapiens@watson.wustl.edu
                                                                                              Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA

    Genome Center

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                                                                                                                                                                                                                                                                                                                                                                                                      Louis,
                                                                                                                                                                                                                                                                                      Louis,
                                                                                                                                                                        USA
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

restriction digest

clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence may not represent the entire insert of this

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misc_feature
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The clone sequenced to the left is RP11-36B15; the clone sequenced to the right is RP11-77C12, 2000 bp overlap. Actual end of this clone is at base position 12410 of RP11-177C12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and Coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping, Department of Genetics, Washington University, St. Louis
MC. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VECTOR:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence of AC009566 has been incorporated into AC108022
Location/Qualifiers
                  /rpt_
6188.
                                                                                                                                                                                                                                                                                                                               /note="similar to Homo sapiens EST BI020745 (NID:g14427375)" 2689. .2836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pBACe3.6
                                                                                                                                                          /rpt_family="MIR"
4513. .4550
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1495.
/note="match to EST BE172154 (NID:g8634880)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to Homo sapiens EST BE069322 (NID:98413972)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="match to EST BF734110 (NID:g12059346)"
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329. .510
                                                                                                                                                                                                                                                                                                                                                                                                                                          note="match to EST
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/db_xref="taxon:9606"
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                                _family="MIR"
                                                                   _family="MaLR"
                                                                                                                                                                                                             _family="MIR"
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                                                               Best Local Similarity:
Query Match:
              US-10-008-355-26 (1-9) x AC108022 (1-162609)
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/rpt_family="L1"
6343. .6534
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13268. .13339
                                                                                                                                                                                                           /rpt_family="Alu"
19184. .19456
                                                                                                                                                                                                                                                                                /rpt_family="MER1_type"
17867. .17961
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15257. .15567
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10967. .11016
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10662
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10337. .10648
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[3062. .13216
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3292. .8347
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9. .14373
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                                                 Gaps:
                                                                   Mismatches: Indels:
                                                                                                     Conservative:
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FEATURES

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AUTHORS
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                     Alignment Scores:
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                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consensus quality: 163223 bases at least Q40
Consensus quality: 164704 bases at least Q30
Consensus quality: 165029 bases at least Q30
Consensus quality: 165029 bases at least Q20
Estimated insert size: 179000; agarose-fp estimation
Quality coverage: 8.17 in Q20 bases; agarose-fp estimation
Quality coverage: 8.78 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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AC108085.1 GI:18369931
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                                                                            /clone="CTD-2210F7"
/clone_lib="CalTech human
32702 c 32339 g 48053
                                                                                                                                       /chromosome="5"
                                                                                                                                                            1. .166978
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                                                                                                                                                                                                                       Location,
                                                                                                                                                                                                                                    1111: contig of 1111 bp in length
1231: gap of unknown length
2531: contig of 1320 bp in length
2631: gap of unknown length
404: contig of 1453 bp in length
4184: gap of unknown length
50656: contig of 46472 bp in length
50756: gap of unknown length
101216: contig of 50460 bp in length
101316: gap of unknown length
101316: gap of unknown length
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t 563 other
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AC036185
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US-10-008-355-26 (1-9) x AC108085 (1-166978)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission

Direct Submission

Submitted (07 APR-2000) Whitehead Institute/MIT Center for Genome Submitted (07 APR-2000)

Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 21, 2000 this sequence version replaced gi:7523854. All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

Smit, A.F.A. & Green, Canama Center
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1 (bases 1 to 171279)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

"ama saniens chromosome 4, clone RP11-679B6
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Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reassembly program: Phrap; version 0.960731 Consensus quality: 163254 bases at least Q40 Consensus quality: 166954 bases at least Q30 Consensus quality: 168680 bases at least Q30 Insert size: 170000; agarose-fp
                                                                                                                                                                                                                                                                                    Center project name: L9247 Center clone name: 679_B_6
                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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Quality coverage: 7.1 in Q20 bases; agarose-fp
Quality coverage: 7.1 in Q20 bases; sum-of-contigs
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4209 7507: contin ~f
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7508 7607: gap of 100 bp
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13870 13969: gap of 100 bp
13970 20810: contig of 6841 bp in
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                                        /note="assembly_fragment"
61627. .75529
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2936. .4108
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20911. .28893
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13970. .20810
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Query Match:
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                                                                   AUTHORS
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                                                                                                                                                                       Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Collins, S., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Garand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Karatas, A., Klain, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Klein, J., Larocque, K., Lamazares, R., Landers, T., Lehoczky, J., Klein, J., Leu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Minoya, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollvar, T. M., Ollver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trajilio, J., Ye, W.J., Volner, J., Zimmer, A., and Zody, M.
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                Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
                                                                                                               Submitted (04-MAY-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 8, clone RP11-131K16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 174253)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
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Young,G., Zainoun,J., Zimmer,A. and Zody,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 Consensus quality: 156518 bases at least Q40 Consensus quality: 165902 bases at least Q30 Consensus quality: 169236 bases at least Q20 consensus quality: 169236 bases at least Q20
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Center clone name: 131_K_16
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3335 3434: gap of 1(
3435 5627: contig of
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33 9592: gap of 100 bp

11429: contig of 1837 b

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//53: contig of 2
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36984 37083: gap of 100 bp
37084 41557: contig of 4474 bp
41558 41657: gap of 100 bp
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117423: contig of 10435 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            $875: gap of 10
52390: contig of 5
$490: gap of 5
57638: contig of 5
738: gap of 10
65255: contig of 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /523: gap of 
[25991: cont
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06888: contig of 8288 k
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98500: contig of 9823 bp in length
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COMMENT

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misc_feature 28293. 33574

misc_feature 32675. 36983

misc_feature 37084. 341557

/note="assembly_fragment"
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Result
No.
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Maximum DB seq
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Perfect score:
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      Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
      length: 0
length: 2000000000
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mane:*
8: sp_organell:
9: sp_phage:*
10: sp_phage:*
11: sp_rodent::
12: sp_virus:*
13: sp_vertebr:
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sp_rvirus:*
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38.381 Million cell updates/sec
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Q04186 staphylococ Q9ajx0 staphylococ Q9ajx0 staphylococ Q9pc94 xylella fas Q47809 enterococcu Q9mg8 rhizobium l Q8ve75 mus musculu Q9d219 mus musculu Q9d219 mus musculu Q9d219 anabaena sp Q8xhm4 clostridium Q9zdx8 rickettsia Q62314 mus musculu Q92j35 rickettsia
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Q99v45 staphylococ
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Q53782	Q9KH49	Q99T60	Q9FD08	Q9KH51	Q9LA54	Q9LA58	Q8RY22	Q9SRP2	Q9FYL4	Q8RE47	Q9E960	Q66149	Q89504	Q9KLD4	Q9RTZ8	Q9FMX1	Q8TZS8	Q8QR15	Q98в89	P96151	074325	Q9P7S1	Q9LK70	Q8VA04	094891	Q8YFB1	Q9A9N9	Q92LB9
	Q9kh49 staphylococ		Q9fd08 staphylococ	Q9kh51 staphylococ	 Q91a54 escherichia 	Q91a58 escherichia	Q8ry22 arabidopsis	Q9srp2 arabidopsis	arabidops	Q8re47 fusobacteri	Q9e960 cocksfoot m	-	cocksfoot		-				9			n5	0	**	colletotri	brucella m		Q92lb9 rhizobium m

ALIGNMENTS

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Q9FBG1
ID Q9FBG1 PRELIMINARY;
AC Q9FBG1;
DT 01-MAR-2001 (TrEMBLrel. 16, C)
DT 01-MAR-2002 (TrEMBLrel. 20, L)
DT 01-MAR-2002 (TrEMBLrel. 20, L)
                                                            RESULT 1
Query Match
Best Local Similarity
Matches 10; Conserv
                                                      "Characterization of the gene encoding glutamyl endopeptide Staphylococcus warneri M.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; A2293885; CAC06168.1; -.
MEROPS; S01.269; -.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR0001256; Ser_protease_V8.
Pfam; pe00089; trypsin; 1.
PFINTS; PR00839; V8PROTEASE.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00673; V8PSOTEASE.
NART; PS000673; V8PSOTEASE.
NART; PS00673; V8PSOTEASE.
NART; SM00020; Tryp_SPC; 1.
PROSITE; PS00673; V8PSOTEASE.
NART; SM00020; Tryp_SPC; 1.
PROSITE; PS00673; V8PSOTEASE.
NART; SM00020; Tryp_SPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus warneri.
Bacteria; Firmicutes; B
Staphylococcus.
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                                                                                                                                                                                                                                                                                                              Submitted (AUG-2000) to the
                                                                                                                                                                                                                                                                                                                               Kakikawa M.;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
   Conservative
               100.0%; Score 54; DB 2; Length 316; 100.0%; Pred. No. 0.15;
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                                                                                                                                                                                                                                             gene encoding glutamyl endopeptidase
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Best Local
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01-JUN-2001
                                                                                                                                                                                                                                                                                                                 Q04186;
Q04186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_proteas_V8.
Ffam; PF00089; tryps1n; 1.
PRINTS; PR00839; VPBROTEASE.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS0040; TRYPSIN_DOM; 1.
PROSITE; PS00672; V8_HIS; 1.
PROSITE; PS00673; V8_SER; 1.
PROSITE; PS00673; V8_SER; 1.
Hydrolase; Protease; Serine protease; Complete proteome.
SEQUENCE 342 AA; 36977 MW; 5AEF42DCE01C4B24 CRC64;
                                                                                                                                                                               Staphylococcus aureus
                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update
Glutamic acid specific protease prepropeptide (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES-S.aureus (strain Mu50), and S.aureus (strain N315);
MEDLINE-21311952; PubMed-11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba
Hattori M., Ogasawara N., Hayashi H., Hiranatsu K.,
                                                       SEQUENCE FROM
                                                                                                                                    Staphylococcus.
                                                                                                                                                          Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315). Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, La
01-JUN-2002 (TrEMBLrel. 21, La
Serine protease, V8 protease,
SSPA OR SAV1048 OR SA0901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q99V45
     Matsumoto
                                                                                                          NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole genome sequencing of meticillin-resistant Staphylococcus aureus.";
                             Yoshikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; S01.269;
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1 TGGNSGSPVF 240
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                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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N.A.
Tsuzuki H., Fujiwara
Shin M., Yoshida N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                          Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17, Created)17, Last sequence update)21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 54; DB 1
Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glutamyl endopeptidase.
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                     ...
  T., Nakamura
Teraoka H.;
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                                                                                                                                                                                                                                                                                                                                         357
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                                                                                                                                                    group;
                                                                                                                                                                                                                                 update)
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                                                                                                                                                          Bacillales;
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                             Iwamoto H.
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RESULT 5

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Q9PC94 PRELIMINARY; Q9PC94; 01-OCT-2000 (TrEMBLrel. 15,

Created)

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RESULT
Q9AJX0
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                                                                                                                                               Query Match
Best Local S
Matches 9
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Best Local S
Matches 10
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Q9AJX0,
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00673; V8_HIS; 1.
PROSITE; PS00673; V8_SER; 1.
PROSITE; PS00673; V8_SER; 1.
PROSITE; PS00673; V8_SER; 1.
POTENTIA
SEQUENCE 357 AA; 38651 MW; 58AA9A
                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000126; Ser_proteas_V8.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2001) to the EMBL; AJ305145; CAC27157.1; HSSP; P09331; 1EXF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00089; trypsin; 1. PRINTS; PR00839; V8PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 1121:221-228(1991). EMBL; D00730; BAA00630.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50240; TRYPSIN_DOM; PROSITE; PS00673; V8_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dubin G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000126; Ser_proteas_V8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0839; V8PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S01.269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; S01.269;
   167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis extracellular serine proteinase.";
submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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                                      2 GGNSGSPVF 10
GGNSGSPVF 175
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                                                                                                                                                   Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serine protease;
                                                                                                                                                                                                                                                                                                      217 AA;
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                   217
23667
                                                                                                                                                                                      90.7%;
100.0%;
                                                                                                                                                                                                                                                                                                   MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
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                                                                                                                                                                                                                                                                                           POTENTIAL.
EXTRACELLULAR SERINE PROTEINASE.
; FB9B886D453B8BB7 CRC64;
                                                                                                                                                                                      Score 49;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58AA9A4E371E2577 CRC64;
                                                                                                                                                   Mismatches
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                                                                                                                                                                                      DB 2;
0.79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          group; Bacillales;
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                                                                                                                                                                                                                     Length 217;
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                                                                                                                                                   Indels
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                                                                                                                                               Gaps
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AC 07
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RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Colauto N.B., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Golintoni A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Mondo D.H., Nobrega F.G., Nunes L.R., Oliveira M.A.,
de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA de Silve A.C.R., de Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Genome sequence of the plant pathogen Xylella fastidiosa.";
RD K.M. A.FONZORO I. -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local (
                               STRAIN=OG1-10;
Su Y.A., Clewel
"A gene (sprE)
                                                                                                                                                                                                                                                                                                                                 01-NOV-1996
01-NOV-1996
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                   Q47809;
Q47809;
                                                                                                                                                                                                                          Enterococcus faecalis Bacteria; Firmicutes;
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Simpson A.J.G., Reinach F.C., Arruda P.,
                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                 Enterococcaceae;
                                                                                                                                                                                                                                                                                                    Staphylococcal serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Complete SEQUENCE 716 AA; 79375 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE004008; AAF84693.1; -. MEROPS; S46.001; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xylella fastidiosa
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01-JUN-2002
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647 TGGNSGSPV 655
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nes 9; Conserv
                               gene (sprE) downstream
                                                      Clewell D.B.;
     serine
                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
ownstream of gelE of Enterococcus faecalis OG1-10 proteinase determinant of Staphylococcus aureus
                                                                                                                                                                                              Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.9%;
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                                                                                                                                                                                                                     (Streptococcus faecalis).
Bacillus/Clostridium grou
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1. 01, Last sequence up
1. 21, Last annotation
proteinase homologue.

    Last sequence update)
    Last annotation update)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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EAF086E2315BBDFC CRC64;
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                                                                                                                                                                                                                     group;
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RESULT
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  RR OCC SET DIT AC
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Best Local S
Matches 8
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Best Local
                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Similar to RIKEN cDNA 4632417K18 gene (Fragment).
Nus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae.
                                                                                                                                                                                                                                    Q8VE75;
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01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP002995; BAB48055.1; -. Hypothetical protein; Complete SEQUENCE 289 AA; 31310 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80W860
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PROSITE; PS00672; V8_HIS; 1.
PROSITE; PS00673; V8_SER; UNKNOWN_1.
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InterPro; IPR000126; Ser_proteas_V8.
PRINTS; PR00839; V8PROTEASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical MSL8587.
SEQUENCE FROM N.A
                                       NCBI_TaxID=10090;
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01-MAR-2002
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|224 TGGQSGSPIY
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8; Conserv
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(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 20, Last annotation updat
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                                                                                                                                                                                                                                                          PRELIMINARY;
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70.0%;
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88.9%;
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ure of the
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Pred. No. 7
                                                                  Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                            PRT;
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8947CDDFC6BC0253 CRC64;
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                                                                  Euteleostomi;
; Murinae; Mus
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RESULT
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Best Local Similarity
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RC STRAIN=C57BL/60; TISSUE=SKIN;

RX MEDLINE=21085660; PubMed=11217851;

RX MEDLINE=21085660; PubMed=11217851;

RX MEDLINE=21085660; PubMed=11217851;

RX Altawa K., Ishia A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R.,

RA Altawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Altawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

RA Altawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Fleischmann W., Gaasterland T., Sikaido I., Pesole G., Quackenbush J.,

RA Fleischmann W., Staubhi F., Szuki R., Tomita M., Wagner L., Washio T.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchl P., Lewis S., Matsuo N., Carninci P., de Bonaldo M.F.,

RA Schriml L.M., Staubhi F., Szuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubhi F., Szuki R., Tomita M., Gariboldi M.,

RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,

RA Basaki H., Sato K., Schoenbach C., Seya T., Sakamoto N.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashtzaki Y., Storchi K., F.,

                                                                                                                                                                                               Matches
                                                                                                                                                                                                           Query Match
Best Local :
               Q98KC9;
Q98KC9;
01-OCT-2001
01-OCT-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (DEC-2)
EMBL; BC019638;
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Mus musculus (Mouse).
Mus mosculus (Motazoa; Chordata;
Metazoa; Rodentia;
                                                                                                                                                                                                                                                                          EMBL;
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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01-JUN-2001 (TrEMBLrel.
4632417K18R1k protein.
4632417K18R1K.
    Hypothetical
                                                                                                                                                                                                                                                                            Nature 409:685-690(2001).
EMBL; AK019499; BAB31763.1; -
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ENCE 613 AA; 69948 MW; F
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8; Conserv
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(DEC-2001)
  (TrembLrel. 18, C
(TrembLrel. 18, L
(TrembLrel. 20, L
) (TrembLrel 20, L
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                                                                                                                                                                                              Conservative
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                                                                       PRELIMINARY;
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                                                                                                                                          548
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                                                                                                                                                                                                                                                  69948
                                                                                                                                                                                                          81.5%;
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88.9%;
                                                                                                                                                                                                                                                                                                   of a full-length mouse
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17,
17,
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              Created)
Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation updat
                                                                                                                                                                                             Pred. No. 17;
1; Mismatches
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                                                                                                                                                                                                                      Score 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51FED8CE693AC1B7 CRC64;
                                                                                                                                                                                                                                                 F926114F705A639B CRC64;
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17;
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                                                                                                                                                                                                                     Length 613;
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  RESULT 12
Q8XHM4
ID Q8XHM
AC Q8XHM
DT 01-MA
DT 01-MA
DT 01-MA
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Q8YM87
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Best Local Similarity
Matches 8; Conserv
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Best Local
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Q8XHM4;
Q8XHM4;
01-MAR-2002
01-MAR-2002
01-JUN-2002
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Q8YM87;
01-MAR-2002
01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP00299
Hypothetical
SEQUENCE 10
                                                                                                                                                                                                                                                           "Complete genomic sequence of the filamentous cyanobacterium Anabaena sp. strain PCC 7120."; DNA Res. 8:205-213(2001). EMBL; AP003598; BAB76748.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21082930; PubMed=11214968; Kaneko T., Nakamura Y., Sato S., Asamizu E., Kaneko T., Nakamura Y., Ishikawa A., Kawashim Kishida Y., Kiyokawa C., Kohara M., Matsumoto Mochizuki Y., Nakayama S., Nakazaki N., Shimpo Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                   Hypothetical
SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical ALR5049.
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Rhizobium loti (Mesorhizobium loti).

Bacteria; Proteobacteria; alpha subdivision;

Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21595285; PubMed=11759840; Kaneko T., Nakamura Y., Wolk C.P.,
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=381; [1]
                                                                                                                                                                                                                                                                                                                Nakazaki N., Shimpo S.,
Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mesorhizobium loti.";
DNA Res. 7:331-338(2000)
                                                                                                                           109
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| 442 TGGNNGSTVF
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8; Conserv
(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                   l protein; Complete
169 AA; 17427 MW;
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                                                        PRELIMINARY;
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88.9%;
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Last sequence update)
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Pred. No.
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L; Mismatches
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                                                        PRT;
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Watanabe A., Iriguchi M., Ishikawa A., Kawashima i
Kishida Y., Kohara M., Matsumoto M., Matsuno A., i
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M.,
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteome.
; AC3F2877D0B94C53 CRC64;
                                                        proteome.
0A610CC04EE4C48A CRC64;
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, Kawashima K., Kimura
Matsumoto M., Matsuno A
N., Shimpo S., Sugimotc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
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                                                                                                                             nitrogen-fixing
1;
                                                                                                                                                                                                  Sasamoto
                                                                                                                                                                    asamoto S.,
a K., Kimura
, Muraki A.,
                          Length 169;
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Gaps
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                                           Query Match
Best Local S
Matches 8
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Best Local S
Matches 7
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01-MAY-1999
01-MAY-1999
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteo Rickettsiaceae; NCBI_TaxID=782;
                                                                                                                                                                                                                                                   mitochondria.";
Nature 396:133-140(1998).
-i- SIMILARITY: TO SERINE PROTEASES,
EMBL; AJ235270; CAA14652.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8XGZ60
                                                                                                                                                                                                                                                                                                                        Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Eriksson A.-S., Whinkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-MADRID E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01225; Mur_ligase; 1. Pfam; PF02875; Mur_ligase_C; 1. TIGRFAMS; TIGR01087; murD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:9
EMBL; AP003194; BABB2165.1; -
InterPro; IPR000713; Mur_ligase.
InterPro; IPR004101; Mur_ligase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          orkain=13 / TYPE A;
PubMed=11792842;
Sh;m;~~~
                                                                                                                                          PROSITE; PS50106; PDZ; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                          Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
                                                                                                                                                                                                      InterPro; IPR001478; pDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
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NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99039499; PubMed=9823893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rickettsia
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MURD OR CPE2459.
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es 7; Conserv
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            TGGNSGSPV
                                         8; Conserv
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                                                                                                         Serine protease; C
315 AA; 35033 MW;
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gasawara N., Hattori M., Kuhara S., Hayashi
enome sequence of Clostridium perfringens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             perfringens.
irmicutes; Bacillus/Clostridium group; Clostridia;
es; Clostridiaceae; Clostridium.
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                                           Conservative
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                                                        74.1%;
88.9%;
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70.0%;
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10,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpha subdivision; Rickettsiales;
eae; Rickettsia.
                                                                                                    Complete proteome. W; 2D91A0D54FFBE9A1 CRC64;
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Last annotation update)
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                                                        Score 40;
Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99:996-1001(2002).
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                                         Mismatches
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                                                                                                                                                                                                                                                                         TRYPSIN FAMILY.
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                                                                        Length 315;
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                                         Indels
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Matches 7
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SEQUENCE
Q62314 PRELIMINARY;
Q62314;
Q1-NOV-1996 (TrEMBLrel. 01,
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O62313 PRELIMINANA,
O62313;
O1-NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
O1-NOV-1996 (TrEMBLrel. 19, Last annotation update)
Trans-golgi network integral membrane protein TGN38A
golgi network protein 1) (TGN38 homolog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. P
GOLGI NETWORK. CYCLES BETWEEN THE TRANS-GOLGI NE
SURFACE RETURNING VIA ENDOSOMES (BY SIMILARITY).
-i- TISSUE SPECIFICITY: WIDELY EXPRESSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JUN-2001) to the E
-i- FUNCTION: MAY BE INVOLVED
FROM TRANS-GOLGI NETWORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ICR; TISSUE-BRAIN;
MEDLINE-95301533; PubMed-7540170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Mus musculus (Mouse).
Chordata; Metazoa; Chordata; Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; Transmembrane; Glycoprotein; SIGNAL 1 17 POTENTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BC009143; AAH09143.1; -. MGD; MGI:105080; Ttgn1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D50031; BAA08757.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- MISCELLANEOUS: ALSO FOUND IN STRAINS BALB/C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kasai K., Takahashi S., Murakami K., Nakayama K.
Strain-specific presence of two TGN38 isoforms
                                                                                                       1 TGGNSGSP 8
                                                                                   TGGNSGKP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGASGSPV 196
                                                                                                                                                    l Similarity
7; Conserv
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87.5%;
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ED IN REGULATING MEMBRANE TRAFFIC
                                                                                                                                                    0;
                                                                                                                                                                    Score 40;
Pred. No.
                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
; 95C340C2F4A21EB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
ENDOCYTOSIS SIGNAL (BY SIMILARITY).
6 X 8 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN TGN38A
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PRT;
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Search completed: December 20, 2002, 12:10:18 Job time: 63.6842 secs
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Best Local Similarity
Matches 7; Conserv
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J. B101. Chem. 270:14471-14476(1995).

J. B101. Chem. 270:14471-14476(1995).

-!- FUNCTION: MAY BE INVOLVED IN REGULATING MEMBRANE TRAFFIC TO AND FROM TRANS-GOLGI NETWORK.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. PRIMARILY IN TRANS-GOLGI NETWORK CYCLES BETWEEN THE TRANS-GOLGI NETWORK AND THE CELL SURFACE RETURNING VIA ENDOSOMES (BY SIMILARITY).

-!- TISSUE SPECIFICITY: WIDELY EXPRESSED.
                                                                                                                                                                                                                                                                                  DOMAIN
SITE
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                          Signal; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-ICR; TISSUE-BRAIN;
MEDILINE-95301533; PubMed-7540170;
Kasai K., Takahashi S., Murakami K., Nakayama K.;
"Strain-specific presence of two TGN38 isoforms and absence of TGN41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Trans-golgi network integral membrane protein TGN38B precursor (Trans-golgi network protein 2) (TGN38 homolog).
TGOLN2 OR TTGN2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D50032; BAA08758.1; -. MGD; MGI:105079; Tgoln2.
                                                  140 TGGNSGKP 147
                                                                          1 TGGNSGSP 8
                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Glycoprotein; Repeat; Golgi stack.

1 17 POTENTIAL.
                                                                                                  Conservative
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                                                                                                              74.1%;
87.5%;
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                                                                                                              Score 40; DB 11; Pred. No. 50;
                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL).; 2826FA9E958C5C27 CRC64;
                                                                                                                                                                                                                                                                  POTENTIAL.
CYTOPLASMIC (POTENTIAL).
ENDOCYTOSIS SIGNAL (BY SIMILARITY).
7 x 8 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                    TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38B.
                                                                                                    Mismatches
                                                                                                  1;
                                                                                                                         Length 363;
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Result
No.
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-MODEL-frame+_p2n.model -DEV=x1h
-O-/cgn2_1/USPTO_spool/US10008355/runat_17122002_112337_14581/app_query.fasta_1.398
-OB-Issued_Patents_NA -QFWT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10008355_@CGN_1_117_@runat_17122002_112337_14581 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XAAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Copyright (c) 1993 - 2002
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              US-09-221-017B-726

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US-08-225-224-31

US-08-225-224-31

US-08-722-258-31

US-08-722-258-31

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Compugen Ltd
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Sequence
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T 1 -221-017B-726 -221-017B-726 -221-017B-726 ent No. 6444799 NERAL INFORMATION: APPLICATION: ROSS, Br TITLE OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRE ADDRESSEE: MORRIS STREET: 755 PAGE CITY: Palo Alto STATE: CA COUNTRY: USA ZIP: 94304-1018 ZIP: 94304-1018 COMPUTER READABLE FO MEDIUM TYPE: Disk COMPUTER: IBM Com OPERATING SYSTEM: SOFTWARE: FastSEQ CURRENT APPLICATION UMBER FILING DATE: 23-D CLASSIFICATION NUMBER FILING DATE: 31-D PRIOR APPLICATION DA APPLICATION NUMBER FILING DATE: 31-D PRIOR APPLICATION NUMBER FILING DATE: 31-D PRIOR APPLICATION NUMBER FILING DATE: 31-D PRIOR APPLICATION NUMBER FILING DATE: 30-J PRIOR APPLICATION NUMBER FILING DATE: 10-D APPLICATION NUMBER FILING DATE: 09-A APPLICATION NUMBER FILING APPLICATION DA APPLICATION NUMBER FILING DATE: 10-D	
APPLICATION NUMBER DATE: 30-ALTON NUMBER TO ALTON NUMBER TO AL	777777777777777777777777777777777777777
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221017E VALIS STER OWS Ve	US-08-035-634 US-09-221-017 US-07-723-002 US-07-952-853 US-08-0478-015 US-08-0478-015 US-08-0478-015 US-08-0351-413 US-08-0351-413 US-08-351-413 US-08-351-413 US-08-351-68 US-08-673-768 US-08-673-768 US-08-673-768 US-08-673-768 US-09-091-814 US-09-091-814 US-09-364-539 US-09-364-539 US-09-364-539 US-09-364-539 US-09-364-539 US-09-364-539 US-09-1812-145 US-09-1812-145 US-09-182-145
CLEOTI	-6.634-1 -0.176-118 -0.178-38 -0.02C-5 -853-21 -121-1 -121-1 -131-2 -0.15-1 -0.15-1 -0.15-1 -0.15-1 -0.16-23 -0
DES AND USES THEREOF	88 88 88 88 88 88 88 88 88 88 88 88 88
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	1, Appli 38, App 38, Appli 5, Appli 1, Appli 1, Appli 1, Appli 2, Appli 1, Appli 2, Appli 3, Appli 1,

ATTORNEY/AGENT INFORMATION:

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US-09-221-017B-1045

Sequence 1045, Application US/09221017B

Patent No. 6444799

GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ROSS, Bruce C. TITLE OF INVENTION: P. GIV NUMBER OF SEQUENCES: 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
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LENGTH: 1974 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                               APPLICATION NUMBER: PP15. FILING DATE: 30-JAN-1998
                                                                                                                                                                                  APPLICATION NUMBER: US/09/221,017B FILING DATE: 23-DEC-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                     STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 650-813-300 PET.EFAX: 650-494-0792
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MUKKLOU.
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: 1...1974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: MONTOY, Gladys REGISTRATION NUMBER:
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STRANDEDNESS: double
TOPOLOGY: circular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                              MORRISON & FOERSTER
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PCT/AU98/01023
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Indels:
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                                                 US-10-008-355-26 (1-9) x US-09-134-001C-892 (1-936)
                                                                                             Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                     US-09-134-001C-892
; Sequence 892, Application US/09134001C
; Patent NO. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC;
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
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Best Local Similarity:
                                                                                                                                                Score:
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                                                                                                                            Percent Similarity:
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                                                                                                                                                                                                                                          SEQ ID NO 892
LENGTH: 936
TYPE: DNA
                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
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STRANDEDNESS: double
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2 GlyGlyAsnSerGlySerProVal 9
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FR: 27340-20021.00
                                                                               Gaps:
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Matches:
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Conservative:
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US-09-071-035-427
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US-09-071-035-425
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Best Local Similarity:
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                                                                                                                                Sequence 425, Application US/09071035
Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: Enterococcus
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GENERAL INFORMATION:
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LENGTH: 758 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
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                                                                                                           TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 496
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                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Gen
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
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               COUNTRY:
                             CITY: Rockville
STATE: Maryland
                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 9410 Key West Avenue CITY: Rockville
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                                                             9410 Key West Avenue
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               USA
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                                                                               Human Genome Sciences,
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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Patent No. 5635599
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ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/225,224 FILING DATE: 8-APR-1994 CLASSIFICATION: 530
                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 888 base pairs
TYPE: nucleic acid
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TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTED FUSION PROTEINS
NUMBER OF SEQUENCES: 57
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OPERATING SYSTEM:
SOFTWARE: ASCII
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ZIP: 94105-1493
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                       15280-193
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TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO:

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Best Local Similarity:
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                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION UMBER: WO PCT/US95/04468

FILING DATE: 06-APR-1995

PRIOR APPLICATION DATA:

APPLICATION UMBER: US 08/225,224

FILING DATE: 08-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 015280-193100US

TELEPAN: (415) 576-0300

TELEPAN: (415) 576-0300

INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6011002
GENERAL INFORMATION:
                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLLOGY: linear
40LECTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Pastan, Ira
APPLICANT: Kreitman, Robert J.
APPLICANT: Puri, Raj K.
TITLE OF INVENTION: Circularly Permuted Ligands and
TITLE OF INVENTION: Circularly Permuted Chimeric Molecules
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                MOLECULE TYPE:
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CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/722,258 FILING DATE: 08-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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RESULT 9
US-08-225-224-28
US-08-225-224-28; Sequence 28, Application US/08225224
; Patent No. 5635599
; GENERAL INFORMATION:
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; Sequence 31, Application PC/TUS9504468
; GENERAL INFORMATION:
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Query Match:
                                                                                                                                                                                            US-10-008-355-26 (1-9) x PCT-US95-04468-31 (1-39)
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                                                                                                                                                                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-6600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US O FILING DATE: 08-APR-1994 ATTORNEY/AGENT INFORMATION: NAME: Weber, Ellen L. REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04468
FILING DATE: 07-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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OTHER INFORMATION:
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                                                                                                                       24 ACCGGAGGTAACGGTGGGGCACCT
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Indels:
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Conservative:
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US-08-722-258-28
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                 Patent No. 6011002
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/225
FILING DATE: 8-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: KREITMAN, Robert J.
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTED FUSION PROTEINS
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                                                                                                                                                                         NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                             APPLICANT: Pastan, Ira
APPLICANT: Kreitman, Robert J.
APPLICANT: Puri, Raj K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                          TITLE OF INVENTION: Circularly Permuted
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 42 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                       CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
 OPERATING SYSTEM:
                                                                                      COUNTRY:
                                                                                                          STATE:
                                                                                                                                          STREET:
                                                                                                                                                            ADDRESSEE:
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                                                                       94111-3834
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                                                                                                       California
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                                                                                                                                        E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                      USA
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PC-DOS/MS-DOS
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Matches:
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Indels:
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Chimeric Mo
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Percent Similarity:
Best Local Similarity:
Query Match:
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FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 543-9600
TELEPAX: (415) 543-9643
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Applicat GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 08-APR-1994
                                                                                                                                                                                                                              CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-193100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/225,224 FILING DATE: 08-APR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/04468
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 08-JAN-1997
                                                                                                                                                                                            FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 42 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ThrGlyGlyAsnSerGlySerPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Application PC/TUS9504468
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                                                                                                                                                           US 08/225,224
                                                                                                                                                                                                                                                               Release #1.0, Version #1.30
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                                                                      15280-193-1PC
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               us-08-998-416-856/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 856,
Patent No. 62
                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Meigs J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wendianu, Carinne
APPLICANT: Knechtle, Philipp
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOP
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6239264art1s Corporation
ADDRESSEE: No. 6239264art1s Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                        TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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LENGTH: 42 base pairs
                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO . .
                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                      FILING DATE: 24 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ThrGlyGlyAsnSerGlySerPro 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F: 3054 Cornwallis Road
Research Triangle Park
No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pohlmann, Rainer
Steiner, Sabine
PAG1539UP
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                            DNA (genomic)
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                                                                                                                                                                                                                                                                                                                     24-DEC-1997
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37.00
87.50%
75.00%
77.08%
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Matches:
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Indels:
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Best Local Similarity:
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Patent No. 5459064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/782,372
FILING DATE: 24-OCT-1991
APPLICATION NUMBER: Japanese Pate APPLICATION NUMBER: Application if FILING DATE: October 24, 1990
ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, KARL
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 29900-20
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 677-7522
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                  MOLECULE TYPE: g
ORIGINAL SOURCE:
ORGANISM: Bact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EPSON PC-286 Book t;
OPERATING SYSTEM: MS-DOS 2.11
SOFTWARE: WOLDSTATE:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SHIONOGI & CO., TITLE OF INVENTION: A NO.! NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      576 ACCGGTGGTGGATCTGGAGGACCTATA 550
                                                                         NAME/KEY: signal peptide LOCATION: 323 to 604
                                NAME/KEY: mature peptide LOCATION: 605 to 1270
                                                                                                                                                                                                 ORGANISM: Bacillus licheniformis STRAIN: ATCC NO. 14580
                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 545 middlefield CITY: Menlo Park
                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/035,634
OTHER INFORMATION:
                                                                       IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                LENGTH:
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               [DENTIFICATION METHOD:
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323 to 1270
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                                                                                                                                                                                                                                                     genomic DNA
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37.00
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77.08%
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Application No. 5459064 2-288110
                                                                   by experiment
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               by experiment
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5459064el Protease
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Conservative:
Mismatches:
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Best Local Similarity:
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                  Best Local Similarity:
Query Match:
                                                                 Score:
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                                                  Percent Similarity:
                                                                                Pred. No.:
                                                                                               Alignment Scores:
                                                                                                                                US-08-680-326-118
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                                                                                                                                                                                                                                       TELEFAX: (415) 494-079
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/680
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: //
STREET: //
CITY: Palo Alto
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                     REEFRENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                             NAME/KEY:
LOCATION:
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                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MORRISON & FOERSTER STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GlyGlyAsnSerGlySerProVal 9
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5. 5925733
                                                                                                                                                                                                                                         454 base pairs
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TODARO, GEORGE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOSCH, MARNIX
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                                                                                                                                                            CDS
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                                                                                                                                                                                              linear
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37.00
87.50%
87.50%
   233
36.00
88.89%
66.67%
75.00%
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ASSOCIATED WITH KAPOSI'S SARCOMA AND RETROPERITONEAL
FIBROMATOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xaa at -94 position of amino acid sequence: formyl methionine
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Indels:
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   Gaps:
                               Conservative: Mismatches:
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                  Indels:
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US-09-221-017B-38/c
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Percent Similarity:
Best Local Similarity:
Query Match:
                                                Score:
                                                                              Alignment Scores
                                                                                                              US-09-221-017B-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 38, Application US/09221017B Patent No. 6444799
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR AFFLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ROSS, Bruce C. TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 686 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP11:
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304-1018
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                        MOLECULE TYPE: DN
                                                               No. .
                                                                                                                                                                                                        ANTI-SENSE:
                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                            TELEFAX: 550
TELEFAX: 706141
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                                                                                                                           NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: bov -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 755 PAGE CITY: Palo Alto
                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Monroy, Gladys H
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                        circular
                                                                                                                         misc_feature
1...686
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363
36.00
88.89%
66.67%
75.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                  32,430
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               Conservative: Mismatches:
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Run

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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-O-/cgn2_1/USPTO_spool/US10008355/runat_17122002_112339_14635/app_query.fasta_1.398
-O-/cgn2_1/USPTO_spool/US10008355/runat_17122002_112339_14635/app_query.fasta_1.398
-DB=Published_Applications_NA -QEMT=fastap -SUFETX=p2n.rupb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=20000000000 -USER=US1000815_@CGN 1_1_21_@runat_17122002_112339_14635
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XOAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on:
                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                 Score
      40
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Match
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48
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83.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Published_Applications_NA: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TGGNSGSPV 9
                                                                                                                                                                                                                   /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                Length
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0 US-09-070-927A-261
0 US-09-867-701-1705
0 US-09-764-878-243
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99.214 Million cell updates/sec
 Sequence 1, Appli
Sequence 261, App
Sequence 1705, Ap
Sequence 243, App
                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
US-10-008-355-1
             Percent Similarity:
Best Local Similarity:
                                                 Score:
                                                                                                             US-10-008-355-1
                                                               Pred. No.:
                                                                              Alignment
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APPLICANT: Travis, James

APPLICANT: Potempa, Jan S

APPLICANT: Benbula, Agrieszka

APPLICANT: Benbula, Agrieszka

TITLE OF INVENTION: Dipeptidylpeptidases and Methods Of Use

FILE REFERENCE: 235.004440101

CURRENT APPLICATION NUMBER: US/10/008, 355

CURRENT FILING DATE: 2001-11-08

PRIOR APPLICATION NUMBER: US 60/246,827

PRIOR APPLICATION NUMBER: US 60/246,827

PRIOR FILING DATE: 2000-11-08

NUMBER OF SEQ ID NOS: 26

NUMBER OF SEQ ID NOS: 26
                                                                                                                       SOFTWARE: PatentIn versio
SEQ ID NO 1
LENGTH: 2139
TYPE: DNA
ORGANISM: Porphyromonas
                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/10008355
Patent No. US20020164759A1
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US-09-770-444-591
US-09-770-444-591
US-09-808-701-14
US-09-9808-701-14
US-09-9808-701-3233
US-09-9864-761-3233
US-09-9815-242-8179
US-09-815-242-8179
US-09-9818-242-8179
US-09-9818-242-8179
US-09-9804-761-24491
US-09-9804-761-24491
US-09-9804-761-2787
US-09-9804-761-2787
US-09-9804-761-2787
US-09-764-868-45
US-09-988-842A-1308
US-09-988-842A-1308
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US-09-988-842A-1308
US-09-988-842A-1308
US-09-988-842A-1308
US-09-988-301-326
US-09-988-301-326
US-09-988-301-343-650
US-09-888-343-1415
US-09-888-343-1415
US-09-888-343-1415
US-09-888-343-1416
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              Length:
Matches:
Conservative:
Mismatches:
2139
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Sequence 406, App
Sequence 1415, Ap
Sequence 676, App
Sequence 21097, App
Sequence 21097, App
Sequence 29769, A
Sequence 29769, App
Sequence 989, App
Sequence 4593, App
Sequence 618, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 98, Appl
Sequence 1308, Ap
Sequence 326, Appl
Sequence 21, Appl
Sequence 1945, Ap
Sequence 1943, Ap
Sequence 1944, Ap
Sequence 5, Appli
Sequence 31758, Ap
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Sequence 51, App
Sequence 6501, App
Sequence 14, Appl
Sequence 32, Appl
Sequence 32, App
Sequence 37, App
Sequence 426, App
Sequence 3053, Ap
Sequence 3053, Ap
Sequence 3053, App
Sequence 750, Appl
Sequence 7787, App
Sequence 7787, App
Sequence 45, Appl
Sequence 45, Appl
Sequence 650, App
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-070-927A-261/c
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     US-09-867-701-1705
                                                                                                                                    US-10-008-355-26 (1-9) x US-09-070-927A-261 (1-4951)
                                                                                                                                                                                                                                                                                                                                 ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-070-927A-261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 261, Application US/09070927A
Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 261: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1930
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FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ThrGlyGlyAsnSerGlySerProVal 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Enterococcus NUMBER OF SEQUENCES: 982
                                                             ACCGGCGGTCAATCTGGTTCACCAATC 669
                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 4951 base pairs
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41.00
88.89%
77.78%
85.42%
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Indels:
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                   US-10-001-887-75
                                                                                                                                                                                                                                                                                                                                                 US-09-764-878-243
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US-09-764-878-243/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
; Sequence 75, Application US/10001887
                                         RESULT 5
                                                                                                                                                     US-10-008-355-26 (1-9) x US-09-764-878-243 (1-7441)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: ROSEN et al.
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA121
CURRENT APPLICATION NUMBER: US/09/764,878
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                              Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 428

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 243

LENGTH: 7441

TYPE: DNA

ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1705
LENGTH: 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 243, Application US/09764878 Patent No. US20020090615A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
APPLICANT: HARLOCKER, SUSAN L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: (1)...(450)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                              2023 GGCGGTAACACAGGCAGCCCTGTG 2000
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Matches:
Conservative:
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Matches:
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and Antibodies

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...i.: ...en, Keith R.
...LICANT: Hufbman, Neill
...LICANT: Hurban, Patrick
ITITLE OF INVENTION: Expressed Sequences of Arabidopsis
ITITLE OF INVENTION: thaliana
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
CURRENT APPLICATION NUMBER: 60/178,502
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows
SEQ ID NO 591
LENGTH: 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-008-355-26 (1-9) x US-10-001-887-75 (1-1775)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/001,887
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/244,998
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/252,563
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. US20020155464A1
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Liu, Chenghua TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and FILE REFERENCE: DEX-0269
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Cafferkey, Robert
Sun, Yongming
Liu, Chenghua
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Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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Hamilton, Carol M.
Price, Jennifer L.
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Rameaka, Joshua G.
                                                                                                                                                                                                                                                                                                                                                                                                                              Page, Amy
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Percent Similarity:
Best Local Similarity:
Query Match:
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; ORGANISM: Arabidopsis thaliana
US-09-770-444-591
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LENGTH: 491
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR PEPILOATION NUMBER: 08/346,731
PRIOR PEPILOATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (110)
OTHER INFORMATION: n equals a,t,g,
                                                                     LOCATION: (428)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (458)
                                                                                                                                            LOCATION: (421)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
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LOCATION: (356)
OTHER INFORMATION: n equals a,t,g,
                  OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature LOCATION: (463)
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OTHER INFORMATION: n equals
NAME/KEY: misc feature
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals a,t,g, or
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RESULT 9
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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; LOCATION: (131)..(952)
US-09-808-701-14
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US-09-808-701-14
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APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
Sequence 14943, Application US/09960352 Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 17
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 14
LENGTH: 11114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Jian-Rui
APPLICANT: Xue, Aidong J.
APPLICANT: Ren, Feiyan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chen, Rui-hong
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NO. US20020146757A1el Nucleic Acids
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 790CIP2D
CURRENT APPLICATION NUMBER: US/09/808,701
CURRENT FILING DATE: 2001-03-14
CURRENT FILING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
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                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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26 ACCGGGGGAACGCAGGGCTCCCCAGTA 552
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Chen, Rui-hong
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Matches:
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Indels:
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Indels:
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GENERAL INFORMATION:
GENERAL INFORMATION G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
ITITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACTI
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica x · 1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
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; Sequence 32393, Application US/09864761

; Patent No. US20020048763A1
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; ORGANISM: Bos taurus
; OTHER INFORMATION: C:
US-09-960-352-14943
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CURRENT FILING DATE: 2001-09-24
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                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
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PRIOR FILING DATE: 2001-01-30
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OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00668
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00663
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00662
OR FILING DATE: 2001-01-30
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Percent Similarity:
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Query Match:
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US-09-864-761-32393
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                                                US-10-008-355-26 (1-9) x US-09-974-300-327 (1-534)
                                                                                                Best Local Similarity:
Query Match:
                                                                                                                                                                                                                   ; ORGANISM: Bacillus licheniformis US-09-974-300-327
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                                                                                                                                 Percent Similarity:
                                                                                                                                                      Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods for Monitoring Multiple Gene
TITLE OF INVENTION: Expression
                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 327
LENGTH: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 32393
LENGTH: 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 327, Application US/09974300 Patent No. US20020146721A1
                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-03-27
NUMBER OF FILING DATE: 2001-03-27
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                      TYPE: DNA
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                                                                                                                                                                    No.:
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APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT FILING DATE: 2001-01-30
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             GlyGlyAsnSerGlySerProVal 9
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EXPRESSED IN LUNG, SIGNAL = 1.9 SWISSPROT HIT: 052325, EVALUE 3.70e+00 NT HIT: ABD29040.1, EVALUE 1.00e-122 EST_HUMAN HIT: BE002805.1, EVALUE 1.00e-122
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EXPRESSED IN LUNG,
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Indels:
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Matches:
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RESULT 12
US-09-864-761-15889/c
; Sequence 15889, Application US/09864761
ratent No. US20020048763A1
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us-10-008-355-26 (1-9)
                                                                                Percent Similarity:
Best Local Similarity:
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                                                            Query Match:
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SEQ ID NO 15889
LENGTH: 557
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APPLICANT:
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PRIOR FILING DATE: 2000-09-21
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PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Penn, Sharron G.
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PRIOR APPLICATION NUMBER: PCT/US01/00667
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APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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x US-09-864-761-15889 (1-557)
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Conservative:
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GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.

APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard
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Best Local Similarity:
Query Match:
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: SOFTWARE: FASTSEQ for Windows Version
: SEQ ID NO 4296
: LENGTH: 720
: TYPE: DNA
: ORGANISM: Staphylococcus aureus
US-09-815-242-4296
                                                                                                                                                                                                                             RESULT 14
US-09-815-242-8179
; Sequence 8179, Application US/09815242
; Patent No. US20020061569A1
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haselbeck, Robert
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3053
LENGTH: 2000
TYPE: DNA
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; NAME/KEY: CDS
; LOCATION: (1)...
US-09-815-242-8179
                                                                                                                                                 ; ORGANISM: Arabidopsis thaliana US-09-938-842A-3053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                      Alignment Scores:
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191.078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/269,308
Percent Similarity:
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 8179
LENGTH: 765
TYPE: DNA
ORGANISM: Staphylococcus aureus
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Command line parameters:

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-Q-/cgn2_1/USPTO_spool_VSI0008355/runat_17122002_112336_14573/app_query.fasta_1.398
-DB=N_Geneseq_101002 -QFMT-fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALLIGN=15
-MODE=-LOCAL -QUTFMT-pto -NORM-ext -HEAPSIZE=-500 -MINLEN=0 -MAXLEN=200000000
-USER-US10008355_eCGN_1_0_0*runat_17122002_112336_14573 -NCPU=6 -TCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NES_SCORES=0 -MAIT -LONGLOG -DEV_TIMESUUT=120
-WARN_TIMESUUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987, DAT: *

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SIDS2/gcgdata/geneseq/geneseqn-emb1/NA198, DAT: *

SIDS2/gcgdata/geneseq/geneseqn-emb1/NA199, DAT: *

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Key

Location/Qualifiers

SUMMARIES

37 38 39 40 41 42 42 43 44 45	C 33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	C 2225 200 200 200 200 200 200 200 200 20		8 10 11 10 11 11 11 14 15	C 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Result No.
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Human novel cytoki Drosophila melanog Human novel cytoki Human protein HP10 Human immune/haema Human immune/haema Human immune/haema Kidney injury asso Human cDNA sequenc Drosophila melanog	Human breast cance Human reproductive Human secreted pro Arabidopsis thalia Sequence encoding Pig lung protease	Human ovarian anti Human breast speci Human secreted pro Human colon cancer Human flavoprotein Drosophila melanog	DNA encoding pyrid Nucleotide sequenc Human prostate exp Aspergillus oryzae DNA encoding C. al Human secreted pro Pseudomonas sp Typ	rerococcus fa faecalis EFII rerococcus fa faecalis EFII capsulatus g capsulatus g cerococcus fa man ovarian ca man venena	Staphylococcus aur Protease from S. A Protease from S. A Porphyromonas ging S. epidermidis ope Staphylococcus epi S. epidermidis gen	Description

ALIGNMENTS

AAV75063 RESULT 1 Staphylococcus aureus contig SEQ ID #752. AAV75063; AAV75063 standard; 16-MAR-1999 (first entry) DNA; 1019

Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds. Staphylococcus aureus.

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RESULT 2
AAQ27988
                                                                                                                                                                                                                         US-10-008-355-26 (1-9) x AAV75063 (1-1019)
                                                                                                                                                                                                                                                         Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                              Alignment
                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                 Protease from S. Aureus
                                                                                                                                                                                                                                                                                     Local Similarity:
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                                            11-FEB-1993
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                                                                          AAQ27988;
                                                                                                      AAQ27988 standard;
                                                                                                                                                                                                                                                                                                                                                                            Sequence 1019 BP;
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                                                                      ВP
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used
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mat_peptide
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rne sequences given in AAQ27987-88 encode proteases which were isolated from Staphylococcus aureus strains. The DNA sequences were isolated by PCR using the primer sequences given in AAQ27960-86. The protease specifically cleaves the peptide bond at the C-terminus of the glutamic acid residue in polypeptide.
                              sig_peptide
                                                                                                           Staphylococcus
                                                                                                                                                                                                       11-FEB-1993
                                                                                                                                                                                                                                                                    AAQ27987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel protease prepd. using Bacillus or Saccharomyces host - capable of cleaving peptide bond at carboxyl terminus of glutamic
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                                                                                                                                        Protease; PCR;
                                                                                                                                                                      Protease from S. Aureus ATCC12600.
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                                                                                                                                                                                                                                                                                                                            standard;
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                              /*tag= = = 352..555
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558..1361
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556..1425
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                                                                             Location/Qualifiers
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequences given in AAQ27987-88 encode proteases which were isolated from Staphylococcus aureus strains. The DNA sequences were isolated by PCR using the primer sequences given in AAQ27960-86. The protease specifically cleaves the peptide bond at the C-terminus of the glutamic acid residue in polypeptide.
                                                                                                                                                                                                                                                                                                                                                      1048
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                                                                                                                                                                                                    Dipeptidylpeptidase-7; DPP-7; go DPP-7 inhibitor identification;
                                                                                                                                                                                                                                    Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) coding sequence
                                                                                                                                                                                                                                                              05-SEP-2002
                                                                                                                                                                                                                                                                                                         AAL43635 standard; DNA; 2139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1586 BP; 590 A;
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(UYGE-) UNIV GEORGIA RES FOUND INC.
                     08-NOV-2000; 2000US-246827P
                                         08-NOV-2001; 2001WO-US46782
                                                                                       WO200238742-A2
                                                                                                                                                                   Porphyromonas gingivalis
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/product= "Porphyromonas gingivalis DPP-7"
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                                                                                                                                                                                                   gene; ds; enzyme; amidolytic cleavage;
n; periodontal disease; gingivitis;
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidylepetidase? (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. glugivitis or periodontitis). The present DNA sequence encodes the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated dipeptidylpeptidase useful for identifying inhibitor of the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis
 Nucleic acids encoding useful for vaccinating
                                         WPI; 2001-316495/33.
P-PSDB; AAG81635.
                                                                                                                                                                                                                                                        Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                          03-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Travis J,
                                                                                     Kimmerly WJ;
                                                                                                                                           09-NOV-1999;
                                                                                                                                                                      09-NOV-2000;
                                                                                                                                                                                                                                                                                                                              S. epidermidis open reading frame nucleotide sequence SEQ ID NO:363.
                                                                                                                                                                                                                                                                                                                                                                                      AAH52485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2139 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
                                                                                                                                                                                                   17-MAY-2001
                                                                                                                                                                                                                              WO200134809-A2
                                                                                                                                                                                                                                                                                                                                                                                                                AAH52485 standard;
                                                                                                              (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO
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DB; AAO15205.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potempa JS,
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                      2000WO-US30782
                                                                                                                                           99US-0164258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        544 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.3
48.00
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis -  \begin{tabular}{ll} \end{tabular} \label{eq:coccus}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         543 C;
                                                                                                                                                                                                                                                                                                                                                                                                                BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         565 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1956
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Matches:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        487 T; 0 other;
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RESULT 6
ABN91429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC (II), given in AAG81454 to AAG83120, from staphylococcus (C) and (II) can have antibacterial activity and therefore can be used CC (I) and (II) can have antibacterial activity and therefore can be used CC (I) vaccination. The nucleic actids (I) may be used to produce the CC s. epidermidis polypeptides (II) via the production of vectors (II) cand/or nucleic actids) may then be ccontaining them which are used to produce hosts cells which express the CC polypeptides. The polypeptides (II) (and/or nucleic actids) may then be ccontained to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their catteriation of therefore identify compounds that may be used for the CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA CC polynucleotide sequences from the present invention. AAH55091 to CC AAH55090 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

CC N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, compared to the present specification of the present specification in the disclosure for SEQ ID NO:4454 so even the sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                 P-PSDB;
                                                                                                                                                                   14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                   Staphylococcus antibacterial;
                                                                                                                                                                                                                   13-AUG-1998;
                                                                                                                                                                                                                                                    30-APR-2002
                                                                                                                                                                                                                                                                                    US6380370-B1
                                                                                                                                                                                                                                                                                                                   Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:892
                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABN91429 standard; DNA; 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH52304 to
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                                                                                                                                   (GENO-) GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match:
                                                                  2002-381255/41.
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                                                    ABP38884.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH53970 represent nucleic acids (I) encoding polypeptides in AAG81454 to AAG83120, from Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                 LA,
                                                                                                                                   THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                  epidermidis; open reading frame; ORF; bacterial infection; gene therapy; gene; ds.
                                                                                                                                                                                                                                                                                                                   epidermidis
                                                                                                                                                                   97US-055779P.
97US-064964P.
                                                                                                                                                                                                                   98US-0134001
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43.00
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Matches:
Conservative:
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Indels:
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in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express polypeptides. The polypeptides (II) (and/or nucleic acids) may then used to vaccinate subjects and to raise antibodies against the bacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          и
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В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    frame (ORP) nucleic acid sequences which encode the amino acid sequence given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infection particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.
                                                                       AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used
                                                                                                                                                                 Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus vaccination; er
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S. epidermidis
                                                                                                                                       Claim
                                                                                                                                                                                                                                             Kimmerly WJ:
                                                                                                                                                                                                                                                                                                       09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                    09-NOV-2000; 2000WO-US30782
                                                                                                                                                                                                                                                                                                                                                                  17-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH54330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH54330 standard; DNA; 3189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN90538 to ABN93374 represent Staphylococcus epidermidis open frame (ORF) nucleic acid sequences which encode the amino acid
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                                                                                                                                                                                                                                                                         (GLAX ) GLAXO GROUP LTD
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                                                                                                                                                                                                              2001-316495/33
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                                                                                                                                     Page 1307-1308; 2188pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       us epidermidis SR1 strain; endocarditis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic polynucleotide sequence SEQ ID NO:3694
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                                                                                                                                     English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection; diagnosis;
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   the bacteria
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472.
                                   The proteins can
                                                                                                                Claim
                                                                                                                                      New isolated Enterococcus faecalis polynucleotides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                   Bailey C,
                                                                                                                                                                                                                                                                                                                                                                             04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection; attenuation; antigenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX20213 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA
                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                         12-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX20213;
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                    nfection
                                                                 isolated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences are
present sequence encodes an antigenic polypeptide fragment lated from Enterococcus faecalis. The present invention describes ries, proteins and antigenic polypeptides isolated from E. faecalis. proteins can be used in vaccines for preventing or attenuating an ection caused by a member of the Enterococcus genus in an animal. Year also be used for detecting Enterococcus antibodies in a samply can also be used for detecting Enterococcus antibodies in a samply can also be used for detecting Enterococcus antibodies.
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                                                                                                                                                                                                        AAY00223
                                                                                                              Page '212-213;
                                                                                                                                                                                                                                                   Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  faecalis
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97US-0044031.
97US-0046655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection; vaccine;
                                                                                                         301pp;
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                                                                                                      The present invention provides the protein and coding sequences of a number of polypeptides from Entercococcus faecalis. The proteins can be used as vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal, particularly E. faecalis. The polynucleotide is also useful for preventing or treating E. faecalis
                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis
                                         No . :
                                                                                                                                                                          Claim 1; Page 197-198;
                                                                                                                                                                                                        New genes and polypeptides from Enterococcus faecalis, useful vaccines for preventing, treating or attenuating an infection a member of the Enterococcus genus in an animal, particularly
                                                                                                                                                                                                                                                     WPI; 2002-425450/45.
P-PSDB; ABP43442.
                                                                                                                                                                                                                                                                                   Choi GH,
                                                                                                                                                                                                                                                                                                                                04-MAY-1998;
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                                                                                                infection.
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                                                                                             The present sequence is a coding sequence is a coding sequence.
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06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a gene isolated from Enterococcus faecalis. The present invention describes genes, proteins can and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide
                                                                                                                                                                                                                                                               Sequence 888 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 212; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated Enterococcus faecalis polynucleotides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection
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                   ACCGGCGGTCAATCTGGTTCACCAATC 729
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P-PSDB;
Methylococcus capsulatus.
                                                                  M. capsulatus
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The present invention provides the protein and coding sequences of a number of polypeptides from Enterococcus faecalis. The proteins can be used as vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal, particularly E. faecalis. The polynucleotide is also useful for preventing or treating E. faecalis.
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Micro array; gene; ds; differential expression; gene expression
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                                                                                                                                                                                                                              AAX13198/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel DNA array giving a representation of a number of Methylococous capsulatus genes. The method of the invention is useful for determination of the differential expression of the genes of M. capsulatus, and for studying gene expression on a genomic scale and in gene expression assays of M. capsulatus genes. The sequences shown in ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the
                                                                                                                                                                                                                                                            1661 ACCGGCGGCAACGCTGGCTCGCCG 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-557818/59
 14-NOV-1997;
06-MAY-1997;
                               04-MAY-1998;
                                                                                               Enterococcus
                                                                                                                              Enterococcus faecalis;
                                                                                                                                                                          19-MAR-1999
                                                                                                                                                                                                AAX13198;
                                                                                                                                                                                                                  AAX13198 standard; DNA; 4951 BP
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; Page 497; 678pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                capsulatus genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel DNA array useful for determining differential expression of Methylococcus capsulatus genes, comprises polynucleotides or oligonucleotides representative for a selective number of Methylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200255655-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birkeland NK,
Lillehaug JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JAN-2002; 2002WO-NO00019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                   No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN (TIGR-) TIGR.
                                                    12-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                         thvention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JAN-2001; 2001NO-0000235.
12-JAN-2001; 2001NO-0000239.
                                                                                                                                                                                                                                                                                  1 ThrGlyGlyAsnSerGlySerPro 8
                                                                                                                     attenuation;
                                                                                                                                                                        (first entry)
                                                                                                                                                   faecalis
                                                                                               faecalis.
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97US-0066009
97US-0044031
                               98WO-US08985
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                                                                                                                                                                                                                                                                                                                                                                                                                  363 A;
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85.42%
                                                                                                                 computer readable medium;
                                                                                                                                                   genome
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                                                                                                                                                                                                                                                                                                                                                                                                                  Ç
                                                                                                                                                  contig SEQ ID NO:261.
                                                                                                                                                                                                                                                                                                        (1-2130)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jonassen I, Jensen
isen JA, Fraser CM,
                                                                                                                             detection; Enterococcal infection;
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match: DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   commercial importance. The products can be used to detect the presence of Enterococcus faecalls in samples. They can also be used for disposing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalls, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecals nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
WPI; 2002-122075/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAXI2938 to AAXI3919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                          Algate PA,
                                                                                                                                                                   WO200192581-A2
                                                                                                                                                                                                                          Human; ovarian
                                                                                                                                                                                                                                                     Human ovarian cancer related cDNA clone SEQ ID NO:1705.
                                                                                                                                                                                                                                                                                  17-MAY-2002
                                                                                                                                                                                                                                                                                                             ABL78727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     system can identify fragments of the Enterococcus faecalis genome with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 1248-1251; 2084pp; English
                                                                                                             29-MAY-2001; 2001WO-US17756.
                                                                                                                                         06-DEC-2001
                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                         ABL78727 standard;
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                                                      (CORI-) CORIXA CORP
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                          Harlocker
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                                                                                 2000US-207484P
                                                                                                                                                                                                                                                                                 (first
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                                                                                                                                                                                                                       cancer; ovarian tumour; cytostatic; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1563 A; 981 C;
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                          Jones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a composition (I) comprising: carriers CC and immunostimulants; and a polypeptide (II) of a ovarian tumour CC polypeptide encoded by a polynucleotide (II) having a cDNA sequence CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell CC population of (II), or antigen presenting cells that express (II). CC (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises CC contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount of polynucleotide hybridising to (IV) and comparing the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising CC (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells contacting or (III) is useful for stimulating and/or expanding T cells contacting in tumour cells; and to isolate a full length gene from a cuttable library e.g., a tumour CDNA library using well known
(NOVO ) NOVO NORDISK BIOTECH INC
                                                                                                                                                                                                   expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide -
                                    22-MAR-1999;
                                                                                                                                                                                                                                                                      Multiple gene expression; filamentous fungal cell; EST;
                                                                                                                                                                                                                                                                                                                                          13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                         536/c
AAF07536 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID 1705; 489pp; English
                                                                  22-MAR-2000; 2000WO-US07781.
                                                                                                                                      WO200056762-A2
                                                                                                                                                                      Fusarium venenatum
                                                                                                                                                                                                                                                                                                         Fusarium venenatum EST SEQ ID NO:59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ThrGlyGlyAsnSerGlySerPro
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                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                  9908-0273623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 A;
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                                                                                                                                                                                                                                                                                                                                                                                                            cDNA;
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Indels:
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the global expression of genes from FF cells allows the production competential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be considered. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore compined to changes in culture conditions, environmental stress, spore compined to the stable of the composition of genes can be used to study how FF cells can compensate the control of cells and compensation of cells can compensation of the gene over genomic or can can compensate the control of the gene products to facilitate microarrays based on function of the gene products to facilitate can be used to the results, AAF11248 to AAF11247 represents ESTs from Aspergillus chiques AAF11854 to AAF11874 to AAF11873 represents ESTs from Aspergillus con control of the gene products to facilitate can be considered to AAF11875 to AAF11875 represents ESTs from Aspergillus con services and confidered to AAF11875 to AAF11875 to Trichoderma reesei, which are considered in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NOVO ) NOVO NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86; Page 393-394; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rey MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shuster JR, Kauppinen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clausen IG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s fungal cells
cells and a
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Query Match: Best Local Similarity: Alignment Scores Percent Similarity: No.: 632 40.00 100.00% 87.50% 83.33% 21 Indels: Mismatches: Matches: Conservative: 1127 7 1 0 0

Sequence 1127

BP;

232 A; 356 C;

268 G; 258 T; 13 other;

US-10-008-355-26 (1-9) x AAF07536 (1-1127)

Вb Ş 332 2 GlyGlyAsnSerGlySerProVal 9 GGAGGGAACTCAGGAACACCAGTG 309

Search completed: December 20, 2002, 13:22:54 Job time: 175.474 secs

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Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
          Issued_Patents_AA:*
1: /cgn2_6/ptodata/1
2: /cgn2_6/ptodata/1
3: /cgn2_6/ptodata/1
4: /cgn2_6/ptodata/1
5: /cgn2_6/ptodata/1
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Gapop 10.0 , Gapext 0.5
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Listing first 45 summaries
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
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US-08-332-562A-67
US-08-523-373-23
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US-08-657-192-3
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US-08-657-192-15
US-08-657-192-15
US-08-657-192-15
US-08-657-192-15
US-09-134-001C-3729
US-09-071-035-428
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US-09-071-035-428
US-09-071-035-428
US-09-081-035-428
US-09-081-035-727
US-08-09-081-13
US-07-927-661A-1
US-07-927-661A-1
US-07-927-661A-1
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US-07-927-661A-1
US-07-927-661A-1
US-09-080-756-727
US-09-080-756-728
US-09-080-756-728
US-09-080-756-728
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US-09-033-650-197
US-08-660-963-13
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Sequence 5, Appli
Sequence 6, Appli
Sequence 9, Appli
Sequence 7, Appli
Sequence 15, Appl
Sequence 3729, App
Sequence 428, App
Sequence 428, App
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22, Appl
22, Appl
727, App
728, Appli
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US-08-332-562A-67
Query Match
Best Local Similarity
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Result

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•	Sequence 89, Appl	Sequence 106, App	Sequence 17, Appl		Sequence 8, Appli	Sequence 23, Appl	Sequence 23, Appl	Sequence 23, Appl	Sequence 36, Appl	Sequence 38, Appl	Sequence 69, Appl	Sequence 69, Appl	Sequence 2, Appli	Sequence 4, Appli				

ALIGNMENTS

Title:

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Seque...

Patent No. 598555,

Patent No. 598555,

GENERAL INFORMATION:

APPLICANT: MCKENZIE, Ian F.C.

APPLICANT: HOGARPH, Mark P.

APPLICANT: SCOTT, Bernadette M.

APPLICANT: BONADONNA, Lisa

APPLICANT: HULETT, Mark D.

"TITLE OF INVENTION: FC RECEPTOR FOR IMMUNOGLOBULIN

"TITLE OF INVENTION: 7 RECEPTOR FOR IMMUNOGLOBULIN

"TITLE OF INVENTION: 7 RECEPTOR FOR IMMUNOGLOBULIN
US-08-332-562A-67
                                                      TELEFAX: (202)...
TELEFAX: (202)...
TELEX: 904136
INFORMATION FOR SEQ ID NO: 67
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                 NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 5427
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,457
FILING DATE: 27-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,562A
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3000 K St
CITY: Washington
STATE: D.C.
                                      TYPE: amino acid
STRANDEDNESS: sir
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3000 K Street, N.W.,
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Score 48; DB 2; Pred. No. 0.083;

Length 15;

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Mismatches

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US-08-523-379 22
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                                                                                                                                                   RESULT 3
                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-523-373-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 22:
                             APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CORRESPONDENCE ADDRESS
               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS
                                                                                                                                                                                                     165 TGGNSGSPV 173
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 213 amino acids TYPE: amino acid strandedness: not releving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/523,373 FILING DATE: 05-SEP-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                  INFORMATION:
                                                                                                   Application US/08523373 6037145
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6037145
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                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                        peptide
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                                 PROCESS FOR PRODUCTION OF PROTEIN
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INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001560-2
                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: not rel
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0:
FILING DATE: 05-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 TGGNSGSPV 173
                                 APPLICATION NUMBER: US/O FILING DATE: 05-SEP-1995 CLASSIFICATION: 435
                                                                                                                                                                                              COUNTRY: USA
ZIP: 22314-3187
                                                                                                                                                                                                                                   STREET: 699 Prince CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                        ADDRESSEE: BURNS, JOHN, STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 699 Princ
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TGGNSGSPV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08523373
6037145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 amino acids
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                                                                                                                                                                                                                                                                                       BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
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                                                                                                                                                                                                                                                                                                                                              PROCESS FOR PRODUCTION OF PROTEIN
                                                                      US/08/523,373
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 JP 6-238595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48;
Pred. No. 1
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FILING DATE: 07-SEP-PRIOR APPLICATION DATA:

07-SEP-1994

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; MOLECULE TYPE: peptide
US-08-523-373-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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Best Local Similarity 100.0%;
Matches 9; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08657192
Patent No. 5747321
                                                             TELEFAX: (703) 836-2021
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                              TELEPHONE: (703) 836-6620
                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-170086
APPLICATION NUMBER: JP 7-170086
FILING DATE: 02-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: YABUTA, Masayuki
APPLICANT: OHSUYE, Kazuhitor
TITLE OF INVENTION: MUTANT S
TITLE OF INVENTION: PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 00: TELECOMMUNICATION INFORMATION: TELEPHONE: 703-836-620 TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,
   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 TGGNSGSPV 173
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/657,192
FILING DATE: 03-JUN-1996
CLASSIFICATION: 435
                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States ZIP: 22313-1404
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STATE: Virginia
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                                    STRANDEDNESS:
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                     TOPOLOGY:
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                     linear
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linear
protein
                                single
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-523-373-5
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                                                RESULT
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Patent No.
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,373
FILING DATE: 05-SEP-1995
CLASSIFICATION: 435
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APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
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MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 00 TELECOMMUNICATION INFORMATION:
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NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,
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APPLICANT: Ohsuye, Kazuhiro
                                                                                               289 TGGNSGSPV 297
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ZIP: 22314-3187
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(6) Application US/08523373 6037145
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GENERAL INFORMATION:

APPLICANT:

Yabuta, Masayuki Ohsuye, Kazuhiro

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                                                                                                                                                                                                                                                                                                                            Patent No. 5747321
GENERAL INFORMATION:
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Best Local S
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FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,60
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              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                               APPLICANT: YABUTA, MASAYUKI
APPLICANT: OHSUYE, Kazuhiro
TITLE OF INVENTION: MUTANT S
TITLE OF INVENTION: PROTEASE
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 TGGNSGSPV 297
APPLICATION NUMBER:
                                                                                                                                                       STREET: P.O. Box
CITY: Alexandria
STATE: Virginia
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TYPE: amino acid
STRANDEDNESS: not releva
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: VA
                                                                                                                                        COUNTRY:
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Similarity 100.0%;
9; Conservative 0
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22313-1404
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US/08/657,192
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Pred. No.
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Best Local 9
                                                               TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 836-20 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,37
                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-238595

FILING DATE: 07-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION UMBER: JP 6-296028

FILING DATE: 07-NOV-1994
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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APPLICATION NUMBER: JP 7-170086
APPLICATION NUMBER: 02-UUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
                                               SEQUENCE CHARACTERISTICS:
                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
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LENGTH: 532 amino acids
                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                 NAME: Meuth, Donna M.
REFERENCE/DOCKET NUMBER: 00
                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sin
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STRANDEDNESS:
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                              ENGTH:
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037145
                               532 amino acids
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not relevant
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                           Version #1.30
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RESULT 11
US-09-134-001C-3729,
Sequence 3729, Application US/09134001C
; Patent No. 6380370
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Matches
               GENERAL INFORMATION:
                                                                                                                                                                                                             Query Match
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APPLICANT: Lynn Doucette-Stamm et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 00 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: YABUTA, Masayuki
APPLICANT: OHSUYE, Kazuhiro
TITLE OF INVENTION: MUTANT STAPHYLOCOCCUS AUREUS V8
TITLE OF INVENTION: PROTEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-170086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 TGGNSGSPV 297
                                                                                                                       289 TGGNSGSPV 297
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                                                                                                                                                                               Local Similarity
nes 9; Conser
                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                 1 TGGNSGSPV 9
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                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                               537 amino acids
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P.O. Box 1404
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ilarity 100.0%;
Conservative 0
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Pred. No. 2.8;
0; Mismatches
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Pred. No. 2.
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Query Match
Best Local Similarity
7; Conserv
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                                                                                 US-09-071-035-428
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LENGTH: 311
TYPE: PRT
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                           TELEFAX: (301) 309-85:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
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                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acid
                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
                                                                                                 MOLECULE TYPE:
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                                                                                                               STRANDEDNESS:
TOPOLOGY: lir
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OPERATING SYSTEM: MSDOS ve.
SOFTWARE: ASCII Text
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mes 8; Conser
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                                                                                                                                                                LENGTH:
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                                                                                                                                              amino acid
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               Conservative
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                                                                                                             ss: single
linear
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                                                                                                                                                                                                                                (301)
                                                                                                                                                                amino acids
                                                                                               protein
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                                                                                                                                                                                                                                309-8504
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100.0%; Pr
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                             85.4%;
77.8%;
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                             Score 41;
Pred. No.
               Mismatches
                             DB 4;
17;
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                                              Length 252;
             Indels
             0;
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             Gaps
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RESULT 13
US-09-071-035-426
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; MOLECULE TYPE:
US-09-071-035-426
                                                                                                                                                                                                                                                                    US-09-342-653-7
            CURRENT APPLICATION NUMBER: US/09/342,653
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: 60/092,841
EARLIER FILING DATE: July 14, 1998
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Microsoft Office 97
SEQ ID NO 7
                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Chromatin Associated Proteins
FILE REFERENCE: BB-1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 426, Application US/09071035 Patent No. 6448043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 426:
LENGTH: 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                        224 TGGQSGSPI 232
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OPERATING SYSTEM: MSDOS vea
SOFTWARE: ASCII Text
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CITY: Rockville
STATE: Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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77.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 284;
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; TYPE: PRT; ORGANISM: Homo sapiens US-09-342-653-7
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Search completed: December 20, Job time : 16.6316 secs
                                                                 В
                                                                                                                Query Match
Best Local Similarity
Thes 7; Conserve
                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-090-048-1
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Best Local Similarity /ɔ.v
Thes 6; Conservative
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Patent No. 5523237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Budtz, Peter

APPLICANT: Nielsen, Per M.

APPLICANT: Nielsen, Per M.

TITLE OF INVENTION: PROTEIN PREPARATIONS
                                                                                                                                                                                                                                                                                               TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                NAME: Agris, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/DK92/00036
FILING DATE: 06-TEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agris, Cheryl H.
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                                                            164 GGQSGSPV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: DK 199/91 FILING DATE: 06-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 16 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/090,048 FILING DATE: 16-JUL-1993
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405 Lexington Avenue, 62nd Floor
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Pred. No. 57;
                                                                                                                                                  Score 37; DB Pred. No. 63;
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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-O-/cgn2_1/USPTO_spool/US10008355/runat_17122002_112338_14609/app_query.fasta_1.398
-D-/cgn2_1/USPTO_spool/US10008355/runat_17122002_112338_14609/app_query.fasta_1.398
-DB-EST -OFWT=fastap -SUFFIX-p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-UTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10008355_@CGN_1_1_763_@runat_17122002_112338_14609 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Perfect score:
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

*	AUTHORS H	REFERENCE 1	·z	H	ORGANISM H	SOURCE h	KEYWORDS E	VERSION A	ACCESSION A	ω	DEFINITION z	LOCUS A	AA411980/c	RESULT 1
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.	Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,	1 (bases 1 to 318)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.	EST.	AA411980.1 GI:2070632	AA411980	3', mRNA sequence.	o sapiens	AA411980 318 bp mrNA linear EST 12-AUG-1997		

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TITLE
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COMMENT
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Best Local Similarity:
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TITLE
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contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic positions of the control 
                                                                                                                                                            Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. au Direct Submission of BAC-end sequences from Anopheles Unpublished (2001)
                                                                                                                                                                                                                                                                                                Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BH400391
BH400391.1 GI:17346607
GSS.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2072 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 306.
Location/Qualifiers
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                     African malaria mosquito
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Institute for Genomic Research Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90
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/clone="IMAGE:727252"
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/db_xref="GDB:5924164"
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ699991 371 bp DNA linear HS_5334_A2_G04_SP6E RPCI-11 Human Male BAC Library genomic clone Plate=910 Col=8 Row=M, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: bjloftusetigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University, College Station, Texas 77843-2123, USA using a HindIII
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library PRCI-11. For BAC
library availability, please contact Pleter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 371)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
                                                                                                                                                           401 Queen Anne Avenue North,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                             High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                      99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                              Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ699991.1 GI:5390239
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/db_xref="taxon:7165"
/clone="AG-ND-147H4"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1:
a 79 c 76 g 160 t
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g,J., Zhao,S., Adams,M.D.
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                                                                                                                                                                                                                                                                                 Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shira Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLAM10682 row: 1 column: 23
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Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BG714149.1 GI:13993080
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                                                                                                                                                                                                                                                quality sequence stop: 677.
Location/Qualifiers
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a 88 c 79 g 117 t
/note="Organ: brain; Vector: pBluescriptk (modified pBluescript KS+); Site_1: BamHI; Site_2: Sal.I-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="Plate=910 Col=8 Row=M"
/clone_lib_"RPCI-11 Human Male BAC Library"
                                                                                                       /clone_1ib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
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                                                                                                                                                                  /clone="IMAGE:4797094"
                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity:
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Zea mays
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1 (bases 1 to 279)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stanford University
855 California Ave,
Tel: 650 723 2227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Walbot V
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Maize ESTs from various
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                                                                                                 61
                                                                                                                                                /tissue_type="embryo"
/dev_stage="14, 21, 28, and 35 days after pollination"
/dev_stage="14, 21, 28, and 35 days after pollination"
/lab_host="E. coli SOLR"
/note="Organ: embryo; Vector: pBluescript SK; Site_1: XhoI
: Site_2: EcoRI; Library was prepared by Statagene using
the Uni-ZAP XR system (Stratagene Bh937328-12). Clones
were picked by a Q-bot after blue/white selection
(ampicillin resistance - use 100 micrograms/microliter).
Developed from a pool of equal amounts of RNA from
developing embryos sampled at 14, 21, 28 and 35 days after
pollination of the Illnois High Oil Maize Strain Cycle
90. This closed strain has been selected for high oil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                walbot@stanford.edu
687001 row: G col
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                                                                                               1890s era
a 78 c
                                                                                                 concentration for 90 generations and originates from the 1890s era open pollinated variety Burr's White" 78 c 68 g 72 t
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Zea mays"
/cultivar="Illinois High Oil"
/db_xref="taxon:4577"
/clone_lib="687 - Early embryo from Delaware"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available royalty-free th
IMAGE Consortium (info@mage.llnl.gov)
Insert Length: 389 Std Error: 0.00
Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 7el: 314 286 1800
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Contact: Wilson RK
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Fax: 314 286 1810
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Location/Qualifiers
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                                                                                                                                                                                         same fetus as the fetal lung library, Soares fetal lung
NbHL19W."
121 c 88 g 79 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:1270461"
/db_xref="taxon:9606"
/clone="IMAGE:345086"
                                                                                                                                                                                                                                                                                                                                                                                          /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares_fetal_heart_NbHH19W"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: Jeffrey Green M.D.
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Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                      /note-"Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

206 c 203 g 130 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="phi0B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:4948443"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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human.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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BE794754
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National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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/lab_host="DM10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript: " (Life Technologies).
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321 c 293 g 163 t
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/clone="IMAGE:6339187"
/clone_lib="NIH_MGC_47"
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM801 row: h column: 21
High quality sequence stop: 690.
Location/Qualifiers
                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shira
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                                                                                        found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM11652 row: e column: 11
                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1466)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                              quality sequence start: 71 quality sequence stop: 136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: lung; Vector: pOTB7; Site_1: XhOI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhOI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a 273 c 267 g 248 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
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/clone="IMAGE:3944516"
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                                          Location/Qualifiers
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/tissue_type="small cell carcinoma"
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                   correct orientation)
Seq primer: -40RP fr
                                                                                                                                                                                                                                                                                                                                                                                               MGI:448440
This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the second second self in the second second self in the second seco
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
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IMAGE:722944 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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                                      /organism="Mus musculus'
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:722944"
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/clone_lib="NIH_MGC_95"
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/lab_host="DH10B"
/clone_lib="Soares mouse lymph node NbMLN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 346)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 bp mRNA linear EST 07-MAR-1: mx26c10.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:681330 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                  WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                             High quality sequence stop: 337.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand was primed with a Not I - oligo(dT) primer (5')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; lst strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                      /clone_lib="Soares mouse
/tissue_type="Liver"
/lab_host="DH10B"
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47 c 52 g 49 t
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/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                        /clone="IMAGE:681330"
                                                                                                                                                             /db_xref="taxon:10090"
                                                                                                                                                                                /organism="Mus musculus"
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(Pharmacia), digested with Not I and cloned into the Not
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COMMENT
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BASE COUNT
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
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                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This clone was previously sequenced on the 5' end only, this new
                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
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Mammalia;
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Bonaldo."
a 103 c
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1 92 c
                                                     double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library
                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:681330"
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/tissue_type="Liver"
                                       constructed and normalized by Bento Soares and M.Fatima
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                                          Scores:
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Other_ESTs: va14909.yl
Contact: Marra M/MashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., P.
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., R.
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
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                                                                                                  3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."

107 c · 72 g 117 t 1 others
                                                                                                                                                                                                                                                           /note="Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; lst strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                             /tissue_type="lymph node"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:722944"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares mouse lymph node NbMLN"
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Best Local Similarity:
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Seq primer:
POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: msoares@blue.weeg.ulowa.edu
The sequence tag present in the cDNA between the NotI site and the Oligo-dT track served to identify it as a clone from the normalized adult 12-Day-Embryo library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA964075
456 bp mRNA linear EST 04-Jr UI-R-CO-gw-c-07-0-UI.sl UI-R-CO Rattus norvegicus cDNA clone UI-R-CO-gw-c-07-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 6 (9), 791-806 (1996) 97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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               /lab_host="DHIOB (Life Technologies)"
/lab_host="DHIOB (Life Technologies)"
/note="Vector: p7773D-Pac (Pharmacia) with a modified
/note p1773D-Pac (Pharmacia) with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                norvegicus
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/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Search completed: December 20, 2002, 15:49:00 Job time: 1377.95 secs
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                                                                                                                                                                                                                                                                                                                                                       hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd

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Listing first 45 summaries
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

10	9	80	7	σ	C,	4	ω	2	1	Result No.
48	48	48	48	48	48	48	48	48	48	Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match Length DB
344	344	336	215	214	213	52	52	10	9	Length 1
18	17	13	17	17	17	23	23	23	23	- B
AAW22218	AAR91033	AAR29644	AAR91044	AAR91043	AAR91042	AA015207	AA015206	AA015228	AAO15229	ID
Protein encoded by	Beta-galactosidase	Protease from S. A	V8 mature protease	V8 mature protease	V8 mature protease	Staphylococcus aur	Porphyromonas ging	Porphyromonas ging	Porphyromonas ging	Description

45	44	4.0		3	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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22	77) N	1 (ر د د	22	22	22	22	22	22	22	22	22	13	12	22	16	22	23	20	22	23	23	23	20	23	20	23	22	23	18	18	17	17	13
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Bacillus lichenifo	Bacillus lichenico	-			_	S	Bacillus lichenifo		Bacillus lichenifo						Serine protease SP	Bacillus lichenifo	Interleukin-2 circ	Novel human diagno	Human peptide enco	Kidney injury asso	Human novel cytoki	Herbicidally activ	Human ovarian anti		_	E faecalis EF110 a		aphylococcus	S. epidermidis ope	Porphyromonas ging	encoded	Protein encoded by	Recombinant V8 pro	.das	Protease from S. A

ALIGNMENTS

RESULT 1 AAO15229 Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; active site; DPP-7 inhibitor identification; periodontal disease; gingivitis; Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) active site 2. 05-SEP-2002 (first entry) AA015229; AAO15229 standard; Peptide; 9 16-MAY-2002. WO200238742-A2. Porphyromonas gingivalis. periodontitis.

08-NOV-2000; 2000US-246827P.

08-NOV-2001; 2001WO-US46782.

(UYGE-) UNIV GEORGIA RES FOUND INC.

WPI; 2002-490075/52.

Travis J,

Potempa JS,

Banbula A,

Bugno

Novel isolated dipeptidylpeptidase useful for identifying inhibitor of the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis $\,$

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The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a
                                                                                                                                                             Claim
                                                                                                                                                                                     Novel isolated dipeptidylpeptidase useful for identifying inhibitor the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis -
                                                                                                                                                                                                                                                                                   Travis J,
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                                                                                                                                                                                                                                                                                  Potempa JS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nzyme; amidolytic cleavage; periodontal disease; gingi
                                                                                                                                                                                                                                                                                  Bugno M;
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Similarity 9; Conser

Conservative

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Mismatches

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Indels

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Gaps

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RESULT 3
AAO15206
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                                                                                                   The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidylepetidase 7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents the
                                                                            or periodontitis).
C-terminal region (
(DPP-7) enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; qinai
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                                                    Sequence
                                                                                                                                                                                                                                                                                               Novel isolated dipeptidylpeptidase useful for identifying inhibitor the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-NOV-2001; 2001WO-US46782
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                                                                                                                                                                                                                                                                       Example 6;
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9; Conser
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                                                     ĀΑ;
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                                                                                           Porphyromonas gingivalis
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Pred. No.
            Score 48;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                 A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      periodontal disease; gingivitis;
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                         Length 52;
                                                                                           dipeptidylpeptidase-7
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TGGNSGSPV 9

Query Match Best Local Matches

Similarity 9; Conserv

100.0%; ilarity 100.0%; Conservative (

0;

Score 48; DB 23; Pred. No. 7.8e+05; ; Mismatches 0;

Length Indels

0;

Gaps

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Sequence

9

AA;

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Claim

4;

Page

32;

65pp;

English

the

The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents an active site region of the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7)

Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide.

amino acid and coding sequence of the peptidylpeptidase-7 (DPP-7) enzyme. The

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RESULT 5
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AAO15207
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated dipeptidylpeptidase useful for identifying inhibitor the dipeptidylpeptidase for protecting an animal from periodontal disease caused by Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; gingivitis;
V8 mature protease (aa1-213).
                             23-MAY-1996
                                                        AAR91042;
                                                                                 AAR91042 standard; Peptide; 213 AA.
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6; Fig 5;
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                                                                                                                                                                                                                         Score 48; DB
Pred. No. 1.4;
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RESULT 6
AAR91043
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Best Local Similarity
Thehes 9; Conserv
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(AAR91043;)

23-MAY-1996 (first anti----
                                                                                                                                                                                                                                                                                                                                                                                                                          A fusion protein, V8D (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides, B is Staphylococcus aureus mature V8 protease lacking the C-terminal repeat region, and L is a linker (AAR91032). It was produced as an inclusion body in Escherichia coli host cells, and was cleaved using the E. coli OmpT protease to yield active V8 protease. Extension of the C-terminal end of the V8 molety of the fusion protein by 1, 2 or 3 amino acids (AAR91042-44) i.e. up to residue Phe-215, also resulted in the formation of inclusion bodies in E. coli. Any further extension gave a soluble product which exhibited protease activity that repressed growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide
                                                                                 Linker peptide; V8 protease; Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escherichia coll; transposon Tn993; aminoglycoside 3'-phosphotransferase.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-NOV-1994;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus strain V8 (ATCC 27733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Linker peptide; V8 protease; Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escherichia coli; transposon Tn903; aminoglycoside 3'-phosphotransferase.
           13-MAR-1996
                                   EP700995-A2
                                                          Staphylococcus
                                                                                                                                              V8 mature
                                                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 8; Fig 14a; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohsuye K, Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP700995-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                       1 TGGNSGSPV 9
||||||||
165 TGGNSGSPV 173
                                                                                                                                                                                                                                                                                                                                                                                                                  host
                                                                                                                                                                                                                                                                                                                                                                                                                  cells.
                                                                                                                                              protease
                                                                                                                                                                                                                                                                                                                                                                                         213 AA;
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94JP-0238595
                                                          aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94JP-0296028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95EP-0306235
                                                                                                                                                (aa1-214).
                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                          strain
                                                                                                                                                                                                                                                                                                                                       0;
                                                          8ν
                                                                                                                                                                                                                                                                                                                                                    Score 48;
Pred. No.
                                                          (ATCC 27733)
                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                             Length 213;
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A fusion protein, V8D (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides, B is Staphylococcus aureus mature V8 protease lacking the C-terminal repeat region, and L is a linker (AAR91032). It was produced as an inclusion body in Escherichia coli host cells, and was cleaved using the E. coli OmpT protease to yield active V8 protease. Extension of the C-terminal end of the V8 molety of the fusion protein by 1, 2 or 3 amino acids (AAR91042-44) i.e. up to residue Phe-215, also resulted in the formation of inclusion bodies in E. coli. Any further extension gave a soluble protein the formation of the protein the formation of the protein bodies in E. coli.
Prodn. of recombinant polypeptide(s) - using host cells transformed
                                                     Ohsuye K,
                                                                                                         07-NOV-1994;
07-SEP-1994;
                                                                                                                                               06-SEP-1995;
                                                                                                                                                                                                    EP700995-A2
                                                                                                                                                                                                                            Staphylococcus aureus strain V8
                                                                                                                                                                                                                                                   Linker peptide; V8 protease; Staphylococcus aureus; recombinant protein; fusion protein; beta-galactosidase; Escherichia coli, transposon Tn903; aminoglycoside 3'-phosphotransferase.
                                                                                                                                                                                                                                                                                                                                                                          AAR91044;
                                                                                                                                                                                                                                                                                                                                                                                                  AAR91044 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 8; Fig 14b; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prodn. of recombinant polypeptide(s) - using host cells transformed
with a gene coding for the desired polypeptide fused to a protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohsuye K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-1994;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-1995;
                                                                                                                                                                          13-MAR-1996
                                                                                                                                                                                                                                                                                                                    V8 mature protease (aa1-215).
                                                                                                                                                                                                                                                                                                                                                23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product which exhibited protease activity that repressed growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SUNR ) SUNTORY LTD
                                                                             (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TGGNSGSPV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  host cells.
                            1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGNSGSPV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 100
9; Conservative
                                                   Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yabuta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 AA;
                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                       94JP-0296028
94JP-0238595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94JP-0296028
94JP-0238595
                                                                                                                                               95EP-0306235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95EP-0306235
                                                                                                                                                                                                                                                                                                                                                                                                 Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.0%;
                                                                                                                                                                                                                                                                                                                                                                                                  215 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48;
Pred. No.
                                                                                                                                                                                                                          (ATCC 27733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 8
AAR29644
ID AAR2
XX AAR2964
AC AAR2
XX Prot
XX A Rept
FT Prot
FT Prot
FT Prot
FT Prot
XX Pro
D3-A
     PT PT PT PT CCCCXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
The sequences given in AAR26842 and AAR29644 are proteases which was isolated from Staphylococcus aureus strains. The DNA sequences encoding these proteins were isolated by PCR using the primer sequences given in AAQ27960-86. The protease specifically cleaves the peptide bond at the C-terminus of the glutamic acid residue in polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A fusion protein, V8D (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides, B is Staphylococcus aureus mature V8 protease lacking the C-terminal repeat region, and L is a linker (AAR91032). It was produced as an inclusion body in Escherichia coli host cells, and was cleaved using the E. coli OmpT protease to yield active V8 protease. Extension of the C-terminal end of the V8 moiety of the fusion protein by 1, 2 or 3 amino acids (AAR91042-44) i.e. up to residue Phe-215, also resulted in the formation of inclusion bodies in E. coli. Any further extension gave a soluble product which exhibited protease activity that repressed growth of the bost calls.
                                                                                                    Disclosure; Page 15-16;
                                                                                                                              acid residues in polypeptide(s)
                                                                                                                                             Novel protease prepd. using Bacillus or Saccharomyces capable of cleaving peptide bond at carboxyl terminus
                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                 03-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR29644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR29644 standard; Protein; 336 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 8; Fig 14c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with a gene coding for the desired polypeptide fused to a protective
                                                                                                                                                                                                                                                           20-FEB-1990;
                                                                                                                                                                                                                                                                                                                                            JP04211370-A
                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-FEB-1993
                                                                                                                                                                                                                              (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Госат
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TGGNSGSPV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGNSGSPV 173
                                                                                                                                                                                                     1992-304938/37
                                                                                                                                                                                    AAQ27988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S. Aureus
                                                                                                                                                                                                                                                           90JP-0040398
                                                                                                                                                                                                                                                                                                                                                                                                                                                          aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amplify;
                                                                                                                                                                                                                                                                                     91JP-0024633
                                                                                                                                                                                                                                                                                                                                                                       /label= Signal_peptide
69..336
/label= Protease
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                  25pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                             of gl
                                                                                                                                             glutamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                          were
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RESULT 9
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                  οy
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В
                                       Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric
Chimeric
                                                                                                            Fusion proteins (AAR91033 and AAR91034) were constructed comprising an Escherichia coli beta-galactosidase derivative (protective polypeptide) fused at its C-terminal end to the S. aureus mature V8 protease without or with the repeat region. The constructs were inserted into vector pG97S4DhCT(G)R6, yielding pV8RFT(-) and pV8RFT(+), respectively. Both constructs yielded active protease
                                                                                                                                                                                                       Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide
                                                                                                                                                                                                                                                                      Ohsuye
                                                                                                                                                                                                                                                                                                              07-NOV-1994;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                              06-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta-galactosidase-V8 protease fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR91033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR91033 standard; Protein; 344 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                 Sequence
                                                                                                                                                                                    Example 2; Page 12-13; 44pp; English.
                                                                                                                                                                                                                                                  WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                       EP700995-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V8 protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAY-1996
                                                                                                                                                                                                                                                                                          (SUNR ) SUNTORY LTD
                                                                                                    when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233
289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TGGNSGSPV 9
                   1 TGGNSGSPV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGNSGSPV 241
TGGNSGSPV
                                                                                                   expressed
                                                                                                                                                                                                                                                                      ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tease; Staphylococcus aureus; recombinant prote
protein; beta-galactosidase; Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli; Staphylococcus aureus strain V8 (ATCC 27733).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               336
                                                                                                                                                                                                                                                                     Yabuta M;
                                                                                344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
297
                                                                                                   in E. coli JM101 transformants.
                                                                                                                                                                                                                                                                                                              94JP-0296028.
94JP-0238595.
                                                                                                                                                                                                                                                                                                                                              95EP-0306235
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "beta-galactosidase region" 125..344
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                   "mature V8 protease without the repeat
                                                                                                                                                                                                                                                                                                                                                                                                        region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                        0;
                                       Score 48; DE
Pred. No. 9.7
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB : Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                             DB 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13;
                                                          17;
                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 336;
                                                          Length. 344;
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                     Gaps
                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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RESULT 10
AAW22218
                                                                                                                                                                                                                The invention relates to new mutant Staphylococcus aureus V8 proteases which have enzyme activity even under environmental conditions which protein denaturation. The mutants are based on 3 truncated V8 proteases lacking 48 (AAW22218), 56 (AAW22219) or 53 (AAW22220) amino acids from the C-terminal of the wild type protease. The mutants also contain amino acid substitutions, especially D44E, N71S and/or R147K. The protein sequence shown here represents a chimaeric protein comprising a truncated Staphylococcus aureus V8 protease lacking the prepro and C-terminal 48 amino acids linked, via a synthetic linker, downstream of the E. coli beta-galactosidase. The S. aureus portion of the chimaera was amplified by the primers AAT/3254-5 from wild type sequence. The coding sequence was then used to generate mutants of the V8 protease which retain their levels of activity in the presence of a higher concentration of protein denaturant e.g. 5 M urea.
                                                                                      Matches
                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutant; Staphylococcus aureus; V8 protease; enzyme; denaturation; primer; truncation; wild type; PCR; polymerase chain reaction; amplification; proteolytic activity; fusion protein; beta-galactosidase; urea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW22218 standard; Protein;
                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 13-14; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus V8 protease mutants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-013693/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohsuye K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW22218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP745669-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUNR ) SUNTORY LTD.
                                                                                                      Local
                                          1 TGGNSGSPV 9
TGGNSGSPV 297
                                                                                    Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
                                                                                                                                                                          344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to denaturation
                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95JP-0170086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96EP-0303939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         уd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "E. coli beta-galactosidase
101..120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125..344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "synthetic R6 linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pV8RPT(-) construct.
                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344
                                                                                      0
                                                                                    Score 48; DE
Pred. No. 9.7
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aureus V8
                                                                                                  ).7;
                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with increased
                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protease portion'
                                                                                                                              Length 344;
                                                                                      Indels
                                                                                      0;
                                                                                    Gaps
                                                                                      0;
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В Š

RESULT 11

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RESULT 12
AAR91034
  В
                                                                                                                                                           δõ
                                                                                                                                                                          Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                           The sequences given in AAR26842 and AAR29644 are proteases which we isolated from Staphylococcus aureus strains. The DNA sequences encoding these proteins were isolated by PCR using the primer sequences given in AAQ27960-86. The protease specifically cleaves the peptide bond at the C-terminus of the glutamic acid residue in
 Key
                Chimeric
                      Chimeric
                                            V8 protease;
                                                           Beta-galactosidase-V8
                                                                                                        AAR91034 standard;
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                      Novel protease prepd. using Bacillus or Saccharomyces host - capable of cleaving peptide bond at carboxyl terminus of glutamic acid residues in polypeptide(s)
                                                                          23-MAY-1996
                                                                                                                                                                                                                                                                        Disclosure; Page 13-15; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                        19-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR26842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR26842 standard;
                                                                                                                                                                                                                                                                                                                                           (SHIO ) SHIONOGI & CO
                                                                                                                                                                                                                                                                                                                                                                                                      JP04211370-A.
                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-FEB-1993
                                      fusion
                                                                                                                                                                                                                      polypeptide.
                                                                                                                                                                                                                                                                                                                                                          20-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                             233
                                                                                                                                                                          Local Similarity les 9; Conserv
                                                                                                                                                    1 TGGNSGSPV 9
                                                                                                                                                                                                                                                                                                                      1992-304938/37.
DB; AAQ27987.
                                                                                                                                             TGGNSGSPV
                                     tease; Staphylococcus aureus;
protein; beta-galactosidase;
              Escherichia coli;.
Staphylococcus aureus strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR;
                                                                                                                                                                                                        357 AA;
                                                                                                                                                                          Conservative
                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                            241
                                                                                                                                                                                                                                                                                                                                                          90JP-0040398
                                                                                                                                                                                                                                                                                                                                                                        91JP-0024633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amplify;
                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Signal_peptide 69..358
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aureus ATCC12600.
                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                              100.0%;
                                                           protease fusion
                                                                                                                                                                                                                                                                                                                                           LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus.
                                                                                                        392
                                                                                                                                                                          0;
                                                                                                                                                                         Score 48; DB Pred. No. 10; Mismatches
                                                                                                        ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                     recombinant
Escherichia
                                                           protein.
               8
                                                                                                                                                                                 10;
               (ATCC 27733).
                                                                                                                                                                                        13;
                                                                                                                                                                          0
                                     protein;
                                                                                                                                                                                       Length 357;
                                                                                                                                                                          Indels
                                                                                                                                                                         0;
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                           were
                                                                                                                                                                         0;
                                                                                                                                                                                       RESULT 13
AAR91035
B
                                                                                                                                                                                                                                  ρ
                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 9
                                                          Chimeric
Chimeric
Chimeric
       Cleavage-site
                                   Region
                                                                                Chimeric
                                                                                                                                                   23-MAY-1996
                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-NOV-1994;
07-SEP-1994;
                     Region
                                                                                                                                                                                AAR91035 standard;
                                                                                                                                                                                                                                                                                            when expressed in E.
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP700995-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                 (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                     289 TGGNSGSPV 297
                                                                                                                                                                                                                              1 TGGNSGSPV 9
                                                                                                                                                                                                                                                 l Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   ~
                                                          synthetic;
Staphylococcus aureus
transposon Tn903.
                                                                                Escherichia coli;
                                                                                                                                                                                                                                                                                                                                                                                                                   Yabuta M;
                                                                                                                                                                                                                                                                               392 AA;
                                                                                                                                                                                                                                                100.0%; ilarity 100.0%; Conservative (
                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 94JP-0296028
94JP-0238595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95EP-0306235
                      101..120
                                     1..100
/note=
                                                                                                                                                                                Protein;
                                                                                                                                                                                 532
                                                                                                                                                                                                                                                  0;
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recombinant protein; fusion protein; Escherichia coli; transposon Tn903; aminoglycoside 3'-phosphotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fusion proteins (AAR91033 and AAR91034) were constructed comprising an Escherichia coli beta-galactosidase derivative (protective polypeptide) fused at its C-terminal end to the S. aureus mature V8 protease without or with the repeat region. The constructs were inserted into vector pG9754DhCT(G)M6, Y1elding pV8RPT(-) and pV8RPT(-), respectively. Both constructs yielded active protease when expressed in E. coli JM101 transformants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective polypeptide
                                                                                                                                                                                                                                                                                                                                                                                            Linker peptide; V8 protease; Staphylococcus aureus;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant V8 protease V8D fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 14-15; 44pp; English.
                         /note= "R6 linker" 104..105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "beta-galactosidase 125..392
                                                                                     /note= "beta-galactosidase region"
                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "mature V8 region"
"cleavage site for OmpT protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48;
Pred. No.
                                                                                                                                                                                                                      strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease
                                                                                                                                                                                                                                                                                                                                                                     beta-galactosidase;
                                                                                                                                                                                                                        ٧8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DΒ
                                                                                                                                                                                                                      (ATCC 27733);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT 14
AAW22219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A fusion protein, V8D (AAR91035), has the formula A-L-B-L-C, where A and C are protective polypeptides (derived from Escherichia coli beta-galactosidase and and Tn903 aminoglycoside 3'chosphotransferase, respectively), B is Staphylococcus aureus mature V8 protease lacking the C-terminal repeat region, and L is a linker peptide (AAR91032). The fusion protein is expressed in inactive form in E. coli. It is then recovered, solubilised and cleaved at the linker peptide regions with a protease intrinsic to the host cells, i.e. ompT protease, to allow recovery of V8 protease.
                                                                                Chimeric
Chimeric
                               Key
Region
 Region
                                                                                                                              proteolytic activity;
                                                                                                                                             Mutant; Startruncation;
                                                                                                                                                                                              Protein
                                                                                                                                                                                                                             11-SEP-1997
                                                                                                                                                                                                                                                                                        AAW22219 standard; Protein; 532 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 16-18; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodn. of recombinant polypeptide(s) - using host cells transformed with a gene coding for the desired polypeptide fused to a protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-141021/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohsuye K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SUNR ) SUNTORY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-1994;
07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP700995-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                          289
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                          TGGNSGSPV 297
                                                                                                                                                                                                                                                                                                                                                                                                        TGGNSGSPV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conserv
                                                                                                                           Staphylococcus aureus; V8 protease; enzyme; denaturation; primer; ion; wild type; PCR; polymerase chain reaction; amplification; ytic activity; fusion protein; beta-galactosidase; urea.
                                                                                                                                                                                            encoded by pV8D construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yabuta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       532
                                                                            Staphylococcus
                                                                                               Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94JP-0296028.
94JP-0238595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95EP-0306235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125..335
/note= "V8
336..356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "R6 linker"
339:.340
/note= "cleavage site
307..532
   101..124
                  /note= "E.
                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "aminoglycoside 3'phosphotransferase
region"
                coli beta-galactosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease region"
                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for OmpT protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                portion"
                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                       RESULT 15
AAW22220
γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to new mutant Staphylococcus aureus V8 proteases which have enzyme activity even under environmental conditions which promote protein denaturation. The mutants are based on 3 truncated V8 proteases lacking 48 (AAW22218), 56 (AAW22219) or 53 (AAW22220) amino caids from the C-terminal of the wild type protease. The mutants also contain amino acid substitutions, especially D44E, N71S and/or R147K. The protein sequence shown here represents a chimaeric protein comprising a truncated Staphylococcus aureus V8 protease lacking the prepro and C-terminal 56 amino acids linked, via a synthetic R6 linker, CC downstream of the E. coli beta-galactosidase. Also included downstream of the V8 protease fragment is a second R6 linker and a fragment of the U8 protease fragment is a second R6 linker and a fragment of the S generated by restriction digestion and ligation from the V8RPT(-) sequence (see AAW22218) by using a natural EcoRV site which removed a further 8 amino acid from the C-terminus. This truncated V8 protease, designated V8D, retains its level of activity in the presence of a higher concentration of protein denaturant e.g. 5 M urea.
                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                        Mutant; Staphylococcus truncation; wild type; proteolytic activity; 1
               Chimeric -
Chimeric -
                                                                                                                             Protein
                                                                                                                                                                                                                        AAW22220 standard; Protein; 537
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus V8 protease mutants - with increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-013693/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP745669-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                       11-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                        289
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 9; Conser
                                                                                                                                                                                                                                                                                                                       1 TGGNSGSPV 9
                                                                                                                                                                                                                                                                                                       TGGNSGSPV 297
                                                                                                                         encoded by pV8F construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 16-17; 42pp;
           Escherichia coli.
Staphylococcus au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to denaturation
                                                                                                                                                                                                                                                                                                                                                                                                                                    532 AA;
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96EP-0303939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "t
337..360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "J
125..336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361..532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                            fusion
                                                       aureus; V8 protease; enzyme; denat PCR; polymerase chain reaction; am fusion protein; beta-galactosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "aminoglucoside 3'-phosphotransferase portion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "R6 linker
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                                                                                                                                                                                                          The invention relates to new mutant Staphylococcus aureus V8 proteases CC which have enzyme activity even under environmental conditions which CC promote protein denaturation. The mutants are based on 3 truncated V8 CC proteases lacking 48 (AAW22218), 56 (AAW22219) or 53 (AAW22220) amino CC acids from the C-terminal of the wild type protease. The mutants also CC contain amino acid substitutions, especially D44E, N71S and/or R147K. CC The protein sequence shown here represents a chimaeric protein CC comprising a truncated Staphylococcus aureus V8 protease lacking the CC prepro and C-terminal 53 amino acids linked, via a synthetic R6 linker, CC downstream of the E. coli beta-galactosidase. Also included downstream of the V8 protease fragment is a second R6 linker and a fragment of the CC maninoglucoside 3'-phosphotransferase protein. The chimaeric sequence was generated by restriction digestion and ligation from the V8RP7(-) CC sequence (see AAW22218) by using a natural EcoRV site which removed a CC designated V8F, retains its level of activity in the presence of a CC higher concentration of protein denaturant e.g. 5 M urea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus V8 protease mutants - with increased
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101..124
/note= "R6 linker sequence"
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ALIGNMENTS

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US-10-008-355-26
                                      Sequence 25, Application US/10008355
Patent No. US20020164759A1
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Potempa, Jan S
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APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And
FILE REFERENCE: 235.00440101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0 SEQ ID NO 26 LENGTH: 9
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CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases and Methods Of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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Pred. No. 8.8e+04;
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; SEO ID NO 3
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-008-355-3
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; OTHER INFORMATION: Consensus sequence
US-10-008-355-25
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US-10-008-355-3
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Best Local 9
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                     SEQ ID NO 4
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Best Local (
                                 CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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APPLICANT: Banbula, Agnieszka
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235,00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
UNMBER OF SEQ ID NOS: 26
                                                                                                                                                         APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
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CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
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TYPE: PRT
ORGANISM: Artificial Sequence
LENGTH: 52
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ilarity 100.0%;
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Pred. No. 0.012;
; Mismatches (
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644 TGGNSGSPV 652

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Query Match
Best Local Similarity
Patches 9; Conserve
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                                                                                                               ; TYPE: PRT ; ORGANISM: Porphyromonas gingivalis US-10-008-355-2
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; TYPE: PRT
; ORGANIZM: Porphyromonas gingivalis
US-10-008-355-8
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US-10-008-355-2
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                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Bonbula, Agnieszka
APPLICANT: Banbula, Agnieszka
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases and Methods Of Use
FILE REFERENCE: 255.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT APPLICATION NUMBER: US/00/46,827
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
RUMBER OF SEQ ID NOS: 26
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Matches
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LENGTH: 699
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APPLICANT: Travis, James
                                                                                                                                                                               SOFTWARE: PatentIn version 3.0 SEQ ID NO 2
                                                Matches
                                                            Query Match
Best Local :
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CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
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NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
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APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Staphylococcus aureus
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                                                                                                                                                                 LENGTH: 712
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                                             Local Similarity
nes 9; Conserv
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TGGNSGSPV 9
                                             Conservative
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                                                            Score 48; DB 9
Pred. No. 0.86;
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Pred. No. 0.064;
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; SOFTWARE: PatentIn version 3.0
; SEO ID NO 9
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-008-355-9
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TYPE: PRT
; ORGANISM: Xylella fastidiosa
US-10-008-355-7
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Best Local Similarity
...tches 9; Conserve
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APPLICANT: Trav1s, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases and Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
                                                                                                    Sequence 6, Application US/10008355
Patent No. US20020164759A1
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Patent No. US20020164759A1
                                                                                    GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
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APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
                                              APPLICANT: Travis, James APPLICANT: Potempa, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 26
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                              APPLICANT:
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CANT: Potempa, Jan S
CANT: Banbula, Agnieszka
OF INVENTION: Dipeptidy!peptidases and Methods Of Use
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ilarity 100.0%;
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100.0%; Pred. No. 0.1
tive 0; Mismatches
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Pred. No. 0.87;
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0.87;
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RESULT 11

US-09-864-761-48349
; Sequence 48349, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
   APPLICANT: Penn, Sharron G.
   APPLICANT: Hanzel, David K.
   APPLICANT: Hanzel, David K.
   APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 734
TYPE: PRT
ORGANISM: Shewanella putrefaciens
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Best Local Similarity
Tatches 9; Conserve
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; TYPE: PRT
; ORGANISM: Shewanella putrefaciens
US-10-008-355-6
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Best Local S
Matches 8
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APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
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APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT EATLIANTON NUMBER: US/10/008,355
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
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CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
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APPLICATION NUMBER: GB 24263.6

2000-10-04 IUMBER: US 2000-09-27

US 60/236,359

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APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21
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Best Local S
Matches 6
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NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Lis
SEQ ID NO 48349
LENGTH: 74
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PRIOR
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
OTHER INFORMATION: EST_HUMAN HIT: BE002805.1, EVALUE 8.00e-39
OTHER INFORMATION: SWISSPROT HIT: Q9ZKD2, EVALUE 3.60e+00
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les 6; Conser
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                                                                                                                                                                                                                          Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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NUMBER: US 60/234,687
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Pred. No.
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; ORGANISM: Staphylococcus aureus US-09-815-242-12277
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US-09-815-242-12277
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                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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SEQ ID NO 5351
LENGTH: 240
TYPE: PRT
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SOFTWARE: F8stSEQ for Windows Version 4.0
SEQ ID NO 12277
LENGTH: 254
TYPE: PRT
Query Match
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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  Conservative
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                    77.1%; Score 37; 100.0%; Pred. No.
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19;
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                                                                   OTHER INFORMATION: 1
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PRIOR APPLICATION NUMBER: US 09/632,366
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 49117
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OTHER INFORMATION:
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
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                                 IN BRAIN, SIGNAL = 0.98
IN BT474, SIGNAL = 1.4
IN BONE MARROW, SIGNAL =
IN LUNG, SIGNAL = 0.94
IN FETAL LIVER, SIGNAL = 1.1
IN PLACENTA, SIGNAL = 1.1
IN HELART, SIGNAL = 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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PRIOR APPLICATION NUMBER: PCT/US01/00667
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PRIOR APPLICATION NUMBER: PCT/US01/00666
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Rank, David R.
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             MAP TO AF176315.1

PLACENTA, SIGNAL = EXPRESSED IN BRAIN, SIGNAL = 0.9

EXT_HUMAN HIT: T92522.1, EVALUE SWISSPROT HIT: P23471, EVALUE 1.
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Search completed: December 20, 2002, 12:17:27

Job time: 12.3684 secs
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48
1 TGGNSGSPV 9
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283224 seqs, 96134422 residues
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multifunctional am	gene mastermind pr	۳.	probable proteinas	probable membrane	probable lipoprote	probable lipoprote	wall associated pr	_	hypothetical prote	magnesium transpor	hypothetical prote				

ALIGNMENTS

C;Date: 04-Dec-1996 **sequence_revision 30-Jun-1991 **text_change 18-Jun-1999 C;Accession: A26812; A00966 R;Carmona, C:, Gray, G.L. Nucleic Acids Res. 15, 6757, 1987 A;Title: Nucleotide sequence of the serine protease gene of Staphylococcus aureus, st A;Reference number: A26812; MUID:87316953; PMID:3306605 A;Accession: A26812

N;Alternate names: staphylococcal serine proteinase C;Species: Staphylococcus aureus

glutamyl endopeptidase (EC 3.4.21.19) precursor - Staphylococcus aureus

A; Molecule type: DNA A; Residues: 1-336 <CAR>

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dues.

C;Superfamily: staphylococcal serine proteinase
C;Keywords: hydrolase; serine proteinase
F;69-336/Product: staphylococcal serine proteinase
F;119,161/Active site: His, Asp #status predicted
F;237/Active site: Ser #status experimental
RESULT 2
639873

RESULT 2

RESULT 2

Apporthetical protein sspA [imported] - Staphylococcus aureus (strain N315)

C;Species: Staphylococcus aureus

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C;Date: 10-May-2001 #text
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A; Title: The primary structure of staphylococcal protease A; Reference number: A23824; MUID:78212487; PMID:96922
A; Accession: A00966
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C;Comment: This extracellular proteolytic enzyme preferentially cleaves the peptide b
C;Comment: This enzyme may be distantly related to the trypsin-type serine proteinase
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A;Experimental source: strain V8
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Reference number: A82515; MUID:20365717; PMID:10910347
A; Nature for a complete list of authors see reference number A59328 below A; Accession: G82672.
A; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh
J.D.; Junqueira, M.L.; Kemper, J.E.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins,
A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.
                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-716 <SIM>
A;Cross-references: GB:AE004008; GB:AE003849; NID:g9106961; PIDN:AAF84693.1; GSPDB:GN001
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A;Residues: 1-357 <YOS>
A;Cross-references: GB:D00730; NID:g216970; PIDN:BAA00630.1; PID:g216971 C;Superfamily: staphylococcal serine proteinase
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A; Title: Purification, characterization and gene cloning of a novel glutamic acid-specia; Pixeference number: S21758; MUID:92287954; PMID:1599945
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R; Yoshikawa, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glutamic acid-specific endopeptidase - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
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A; Residues: 1-342 <KUR>
A; Cross-references: GB:BA000018; PID:g13700850;
A:Experimental source: strain N315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision
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hypothetical
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9; Conserv
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TGGQSGSPI 232

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A;Molecule type: DNA
A;Residues: 1-284 <SUY>
A;Cross references: EMBL:Z12296; NID:g43337; PIDN:CAA78168.1; PID:g43338
C;Superfamily: staphylococcal serine proteinase
                                                                                                                                                                                                                                                                                      c;Species: Enterococcus faecalis C;Species: Enterococcus faecalis C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1999 C;Accession: $25140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabat. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AI2436
                                                                                                                                                                                              submitted to the EMBL Data Library, June A;Description: A gene (sprE) downstream A;Reference number: S25140 A;Accession: S25140
                                                                                                                                                                                                                                                                                                                                                             RESULT
S25140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Experimental source: GB:BA000019; PIDN:BAB76748.1; PID:g17134187; GSPDB:GN00179
A;Experimental source: Strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A;Reference number: A59328
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A; Gene: alı
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                                   Similarity 7; Conserv
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8; Conserv
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                                     Conservative
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Sugimoto, M.; Takazawa, M.;
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                                                  Score 41;
Pred. No.
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C:Species: Mus musculus (house mouse)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: A56940
R:Kasai, K.; Takahashi, S.; Murakami, K.; Nakayama, K.
J. Biol. Chem. 270, 14471-14476, 1995
A:Title: Strain-specific presence of two TGN38 isoforms and absence of TGN4
A:Reference number: A56940; MUID:95301533; PMID:7540170
A:Accession: A56940
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R;Kasai, K.; Takahashi, S.; Murakami, K.; Nakayama,
J. Biol. Chem. 270, 14471-14476, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      integral membrane protein TGN38A - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
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R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Nature 396, 133-140, 1998

A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitoch A;Reference number: A71630; MUID:99039499; PMID:9823893

A;Accession: E71729
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C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
                                                                          A; Molecule type: mRNA
A; Residues: 1-363 <KAS>
A; Cross-references: GB: D50031
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A;Experimental source: strain Madrid E
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A; Residues: 1-315 < AND>
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hypothetical protein SPBC1685.05 - fission yeast (Schizosaccharomyces pombe) C:Species: Schizosaccharomyces pombe C:Species: Schizosaccharomyces pombe C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C:Accession: T39521 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A. submitted to the EMBL Data Library, July 1998 A:Reference number: Z21861 A:Recession: T39521 A:Accession: T39521 A:Status: preliminary: translated from GB/EMBL/DDBJ A:Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C;Accession: T50186
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C;Keywords: hydrolase; serine proteinase
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A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: B97729
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A; Residues: 1-996 <BAD>
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A;Gene: SPDB:SPAC23G3.12c
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A; Accession: T50186
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A; Residues: 1-497 < KUR>
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leucine aminopeptidase-related protein VCA0812 [imported] - Vibrio cholerae (strain N169 C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: B82414
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C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002
C;Accession: S63064; S67335
R;De Antoni, A; D Angelo, M; Dal Pero, F.; Sartorello, F.; Pandolfo, D.; Lanfranchi, submitted to the Protein Sequence Database, April 1996
A;Reference number: S63047
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A;Cross-references: GB:AE004409; GB:AE003853; NID:g9658233; PIDN:AAF96710.1; GSPDB:GN001A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                               A; Molecule type: DNA
A; Residues: 1-476 <HEI>
                                                                                                                        A; Reference number: A82035; A; Accession: B82414
                                                                                                                                                                                            R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
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A; Note: YNL123w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, February 1996
A; Description: The DNA sequence of cosmid 14-13b from chromosome XIV of Saccharomyces A; Reference number: S67327
A; Recession: S67335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z71399; NID:g1302053; PID:e239802; A;Experimental source: strain S288C R;d'Antoni, A.; d'Angelo, M.; dal Pero, F.; Sartorello, F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable membrane protein YNL123w - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein N1897
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A;Cross-references: EMB
                                                                                                                                               A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae A;Reference number: A82035; MUID:20406833; PMID:10952301
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A; Residues: 1-997 <DAN>
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A; Residues: 1-997 <DEA>
                                                                                                 A;Status: preliminary
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77.8%;
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A;Experimental source: BAC clone B11B22; strain OR74A
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-!- FUNCTION: PREFERENTIALLY CLEAVES PEPTIDE BONDS ON THE CARBOXYL-TENNINAL SIDE OF ASPARTATE RAID GLUTAMATE.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Asp-|-xaa, Glu-|-xaa-
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2B.
-!- DATABASE: NAME-Worthington enzyme manual;
-!- DATABASE: NAME-Worthington-biochem.com/manual/P/STAP.html".
                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                               EMBL; Y00356; CAA68434.1; -. EMBL; AF309515; AAG45843.1;
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J. Biochem. 56:534-544(1978).
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R., Bast D., de Azavedo J., McGavin M.J.;
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PIR; A26812; PRSASK. MEROPS; S01.269; -.

IPR000126; Ser_proteas_V8

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Lemmens I.H., Kas K., Merregaert J., Van De Ver
"Identification and molecular characterization
gene cluster on human chromosome 11q13.";
Genomics 49:437-442(1998).
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Beccari T.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                  Submitted
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                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                               Holmer L., Pezhman A., Worman H.J.;
"The human lamin B receptor/sterol reductase
Genomics 54:469-476(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                      PubMed=11784322;
                                                                                                                                                                                                                 FUNCTION
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                                                                                       "Cloning and
liver.":
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. J. Blochem. 269:283-290(2002). FUNCTION: Involved in the convecaTALYTIC ACTIVITY: 4,4-dimethy
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nd expression
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V8_SER; 1.
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M.A., Servillo G.;
of sterol Deltal4-r
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N -> D (IN REF. 3).
V -> T (IN REF. 3).
D -> N (IN REF. 3).
EFN -> QFD (IN REF. 3).
ENV -> NEVN (IN REF. 3).
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POTENTIAL.
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Pred. No. 0.2;
0; Mismatches
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to cholest,
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                                                                                                                                                                                     01-OCT-1996 (Rel. 34
01-OCT-1996 (Rel. 34
15-JUN-2002 (Rel. 41
Hypothetical 110.9 k
YNL123W OR N1897
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PROSITE; PS0101
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P53920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
SEQUENCE
                                                                                                  Eukaryota; Fungi; //
Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a clother was a statement the EMBL the European Bioinformatics Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                       SEQUENCE FROM N.A. MEDLINE=97245296; Pubmed=9090055;
                                                                                                                                                                   Saccharomyces cerevisiae (Baker's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sterol biosynthesis; Oxidoreductase; NADP;
de Antoni A., D'Angelo M., Dal
Pallavicini A., Lanfranchi G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                            163 GGNSGNPI 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 colon (mucosal lining), or peripheral blood leukocytes. SIMILARITY: BELONGS TO THE ERG4/ERG24 FAMILY. CAUTION: Ref.1 sequence differs from that shown due to sequencing problems as reported in Ref.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               beta-ol + NADP(+) = 4,4-dimethyl-5-alpha-cholesta-8,14,24-trien-3-beta-ol + NADPH.
SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
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but not detected in pl
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PS01017; STEROL_REDUCT_1;
PS01018; STEROL_REDUCT_2;
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                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                           Ascomycota; Saccharomycotina; Saccharomycetaceae; Saccharomycetaceae;
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75.0%;
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Best Local
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01-OCT-1993 (Rel. 27, L
16-OCT-2001 (Rel. 40, L
Glutamyl endopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae reveals a overlapping open reading frames."; Yeast 13:261-266(1997).
                                                              endopeptidase from Bacillus licheniformis.";
Eur. J. Biochem. 204:165-171(1992).
-i- FUNCTION: SPECIFIC FOR HYDROLYSIS OF PEPTIDES
-CARBOXYL SIDE OF ACIDIC AMINO ACID RESIDUES,
PREFERENCE FOR GLU.
-i- CATALYTIC ACTIVITY: Preferential cleavage: As
                                                                                                                                                                                                                                                  Kakudo S., Kikuchi N., Kitadokoro K., Fujiwara T., Nakamura E., Okamoto H., Shin M., Tamaki M., Teraoka H., Tsuzuki H., Yoshida N., "Purification, characterization, cloning, and expression of a
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.,
STRAIN-ATCC 14580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACLI
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InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00595; PDZ; 1.
SMART; SM00228; PDZ; 2.
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               This
                                                                                                                                                           Svendsen I.,
                                                                                                                                                                        MEDLINE=92155199;
                                                                                                                                                                                     SEQUENCE OF 95-316.
                                                                                                                                                                                                                                          glutamic acid-specific
                                                                                                                                                                                                                                                                                             MEDLINE=93054737; PubMed=1429718;
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                                                                                                                                                                                                                                                                                                                                                            Bacillus licheniformis
Bacteria; Firmicutes; I
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                                                                                                                                             "Isolation and amino acid sequence of a
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                                      SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2B.
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SWISS\text{-}PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                Chem.
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                                                                                                                                                                                                                267:23782-23788(1992)
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                                                                                                                                                                        PubMed=1346764;
                                                                                                                                                                                                                                                                                                                      AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110881
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77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
e precursor (EC 3.4.21.19)
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HME1_MOUSE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HME1_MOUSE STANDARD; PRT; 401 AA. P09065; 01-NOV-1988 (Rel. 09, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Homeobox protein engrailed-1 (Mo-En-1).
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DISULFID
DISULFID
SEQUENCE
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CHAIN
ACT_SITE
           MEDLINE-86079501; PubMed-2416459;
Joyner A.L., Kornberg T., Coleman K.G., Cox
"Expression during embryogenesis of a mouse
homology to the Drosophila engrailed gene.";
Cell 43:29-37(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                   Logan C., Hanks M.C., Noble-Topham S., Provart N.J., Joyner A.L.; "Cloning and sequence comparison of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000126; Ser_proteas_V8.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                "En-1 and En-2, two mouse genes with sequence homology to the Drosophila engrailed gene: expression during embryogenesis."; Genes Dev. 1:29-38(1987).
                                                                                                                                                                                                                                                  SEQUENCE OF 278-401 FROM N.A. MEDLINE-88112776; Pubmed-2892757;
                                                                                                                                                                                                                                                                                                                                                              engrailed genes
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PIR; A45134; A45134.
MEROPS; S01.271; -.
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                                                                                                                        SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                            regions."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                  Joyner A.L., Martin G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 GGQSGSPV 265
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87.5%;
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POTENTIAL.
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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PIR; A24778; A24778.

PIR; S13009; S13009.

PIR; A48423; A48423.

HSSP; P02836; 3HDD.
                                                                                                                                                                                                                                                                                                                                                                                      DNA_BIND SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEBS
         Raguz S., Yaguee E., Wood D.A., Thurs "Isolation and characterization of a
                                                 SEQUENCE FROM N.A. STRAIN-D649;
                                                                                    Eukaryota; Fungi; Basidiomycota; I
Agaricales; Agaricaceae; Agaricus
NCBI_TaxID=5341;
                                                                                                                           Agaricus bisporus
                                                                                                                                               vi-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Cellulose-growth-specific protein precursor
                                                                                                                                                                  01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                            01-NOV-1997
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Q00023;
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PRINTS; PR00026; ENGRAILED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTRANSFAC; T02016; -.
MGD; MGI:95389; En1.
InterPro; IPR000747; Engrailed.
InterPro; IPR001356; Homeobox.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                evolution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00024; HOMEOBOX.
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                                  MEDLINE-93012985;
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                                                                                                                                                                                                                                                                                     238 SGGNAGSP 245
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SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE ENGRAILED HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; PS00027; HOMEULL:; 1
3; PS50071; HOMEOBOX_2; 1
ecn0033; ENGRAILED; 1
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52 87 PRO-RICH.
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73
207
312
401
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                                                                                                         (Common mushroom).
Basidiomycota; Hymenomycetes; Homobasidiomycetes;
                                    PubMed=1398098;
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371
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75.0%;
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POLY-ALA.
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                                                                                                                                                                                                                    PRT;
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                      Thurston C.F.;
          cellulose-growth-specific gene
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RESULT 7
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Best Local S
Matches 6
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DISULFID
CARBOHYD
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Armesilla A.L., Thurston C.F., Yaguee E.;
"CEL1: a novel cellulose binding protein secreted by Agaricus bisporus during growth on crystalline cellulose.";
FEMS Microbiol. Lett. 116:293-299(1994).
1- FUNCTION: PROBABLE GLYCOSYL HYDROLASE ACTIVE ON CELLULOSE.
1- SUBCELLULAR LOCATION: Secreted.
1- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN
1- SIMILARITY: BELONGS TO FAMILY 61 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                               PLYB_AS
Q00205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
            Kester H., Hinnen A., Visser J.;
"Characterization of the Aspergillus regulation of expression.";
Mol. Gen. Genet. 234:113-120(1992).
                                                                                                                                        Aspergillus niger.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JDC-1998 (Rel. 37, Last annotation update)
Pectin lyase B precursor (EC 4.2.2.10) (PLB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00734; CBM_1; 1.
Pfam; PF03443; Glyco_hydro_61; 1.
SMART; SM00236; fCBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M86356; AAA53434.1; -.
HSSP; P00725; 2CBH.
InterPro; IPR000254; CBD_fungal.
InterPro; IPR005103; Glyco_hydro.
                                                 Kusters-Van Someren M., Flipphi M.,
Kester H., Hinnen A., Visser J.;
                                                                            STRAIN=CBS 120.49 / N400;
MEDLINE=92357005; PubMed=1495474;
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=D649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 119:183-190(1992).
[2]

    -!- CATALYTIC ACTIVITY: Eliminative cleavage of pectin to give

                                                                                                                              NCBI_TaxID=5061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use
                                                                                                                                                                                                                                                                                                                           256 SGGNGGSP 263
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                                                                                                                                                                                                                                                             ASPNG
                                                                                                                                                                                                                                                                                                                                                   TGGNSGSP 8
                                                                                                                                                                                                                                                                                                                                                                            Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00562; CBD_FUNGAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 degradation; Hydrolase; Glycosidase; 1 29 POTENTIAL.
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30
262
286
292
303
163
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                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                          320
261
285
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309
319
163
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75.0%;
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CELLULOSE-BINDING (
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                    Score 36;
                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED
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60E2C8080895CA2B CRC64;
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                                     niger pelB
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26;
                                                               Graaff L.,
                                                                                                                                                                                              (PLB)
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ABFA_ASPNG
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Best Local
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Pfam; PF00544; pec_lyase; 1.
Lyase; Signal; Glycoprotein; Multige
SIGNAL 1 20 OR 21 (
CHAIN 21 378 PECTIN
ACT_SITE 255 255 POTENTI
CARBOHYD 128 128 N-LINKE
CARBOHYD 251 251 N-LINKE
CARBOHYD 251 251 N-LINKE
                                                                                                                                                                                                                                Flipphi M.J.A., Visser J., van der Veen P., de Graaff L.H.;
"Arabinase gene expression in Aspergillus niger: indications coordinated regulation.";
Microbiology 140:2673-2682(1994).
-!- FUNCTION: ACTS ONLY ON SMALL LINEAR 1,5-ALPHA-LINKED
-!- FUNCTION: ACTS ONLY OLIGOSACCHARIDES.
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing arabinofuranoside residues in alpha-L-arabinosides.
-!- PARHWAY: INVOLVED IN DEGRADATION OF THE PLANT CELL WALL
                                        use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
STRAIN=CBS 120.49 /
MEDLINE=95093616; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aspergillus niger.
Eukaryota; Fungi; Ascomycota
Eurotiales; Trichocomaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Last a Alpha-L-arabinofuranosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABFA_ASPNG
P42254;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=5061;
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SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European Bioinformatics Institute.
                                                                                                                                                                                              SIMILARITY: BELONGS TO FAMILY 51 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                    POLYSACCHARIDE L-ARABINAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EN
European Bioinformatics Institute. There are no restr
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(Rel. 32, Last sequence update)
(Rel. 33, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=8000538;
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77.8%;
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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PECTIN LYASE B.
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31;
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                                                                                                                                                                                                                                                                                                                                                                      P., de Graaff L.H.;
us niger: indications
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                                                  http://www.isb-sib.ch/announce/
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                                                                              Usage
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                                                                                                                                        collaboration -
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RESULT 10

IRX5_HUMAN STANDARD;

ID IRX5_HUMAN STANDARD;

AC P78411; P78416;

AC P78411; P78416;

CREATER P78416;

CREATER P78416;
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RESULT 9
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Matches 6
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Matches 5; Conserv
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                                                                                Hypothetical SEQUENCE 1
                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 11.7 kDa protein (ORF108).
Orgyia pseudotsugata multicapsid polyhedrosis
Viruses; dsDNA viruses, no RNA stage; Baculov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                 polyhedrosis virus genome.
Virology 229:381-399(1997)
                                                                                                                                                                                                                                              Ahrens C.H.,
Rohrmann G.F
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=97271300; PubMed=9126251;
MEDLINE=97271300; PubMed=9126251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Hydrolase; Gly
                                                                                                   EMBL; U75930; AAC59107.1;
                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ex
                                                                                                                                                                                                                                                                                                            Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=164623;
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                    1 TGGNSGSPV
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TGGRAGNPI
                                                                                                                                                                                                                          sequence of the Orgyia |
hedrosis virus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conserv
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                                                                               al protein.
108 AA; 1
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                                                                               11703 MW;
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75.0%;
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                                                                                                                                                                                                                                     pseudotsugata multinucleocapsid
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N-LINKED
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Pred.
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
4F3E476FF93468AD C
                                                                                80B64CDDE0F24501 CRC64;
                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                 35; DB
No. 12;
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No.
                                                                                                                                                                                                                                                        Evans J.,
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                                                                                                                                                                                                                                                                                                                     Baculoviridae;
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Matches
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DNA_BIND 47 109
DOMAIN 120 126
DOMAIN 254 260
DOMAIN 284 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
STRAIN-ATCC 29342 / M129
                        SEQUENCE FROM
                                                               Mycoplasma pneumoniae.
Bacteria; Firmicutes;
NCBI_TaxID-2104;
                                                                                                                                        Hypothetical lip
MPN592 OR MP250
                                                                                                                                                                                      16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                              MYCPN
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SMART; SM00389; HOX; 1.
SMART; SM00548; IRO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001356; Homeobox.
InterPro; IPR003893; Iroquois_homeo.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:14361; IRX5.
MIM; 606195; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSFAC; T02436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U90309;
HSSP; P41778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U90304; AAB50002.1; -. EMBL; U90309; AAB50007.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell Tissue Res. 296:549-554(1999).
-- -- SUBCELLULAR LOCATION: Nuclear (Probable).
-- -- SIMILARITY: BELONGS TO THE TALE/IRO HOMEOBOX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene, in the human breast.
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Lewis M.T., Ross S., Strickland P.A., Snyder C.J., Daniel C.W.;
"Regulated expression patterns of IRX-2, an Iroquois-class home
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                       16-OCT-2001
                                                                                                                                                                                                                                                                                   YF92_MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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(Rel. 40,
(Rel. 40,
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HOMEOBOX_2; 1.
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Last annotation update)
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Last annotation updat
                                                                                                                                                                                                                                     Created)
                                                                                       Mollicutes; Mycoplasmataceae; Mycoplasma
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G -> A (IN REF. 1;
401F2D865C052AFA
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                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                              precursor (D02_orf521)
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

C STRAIN=ACCC 29342 / M129;

C MEDLINE=96177562; PubMed=8604303;

RA Hilbert H., Himmelreich R., Plagens H., Herrmann R.;

RY "Sequence analysis of 56 kb from the genome of the bac

RY Mycoplasma pneumoniae comprising the dnaA region, the

cluster of ribosomal protein genes.";

cluster of ribosomal protein genes.";
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YF88_MYCPN
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Best Local S
Matches 6
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Q50339;
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
Hypothetical lipopr
MPN588 OR MP254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hilbert H., Himmelreich R., Plagens H., Herrmann R.;
"Sequence analysis of 56 kb from the genome of the bacterium
Mycoplasma pneumoniae comprising the dnaA region, the atp operon and
cluster of ribosomal protein genes.";
Nucleic Acids Res. 24:628-639(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the Inthe European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U43738; AAC43664.1; -. EMBL; AE000025; AAB95898.1; -. InterPro; IPR002414; DUF30/31.
                                                                                                                                                                                    Mycoplasma pneumoniae. Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                      NCBI_TaxID=2104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Lipoprotein; Membrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 24:4420-4449(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Himmelreich R., Hilbert H.,
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                                                                                                                                                                                                                                                                                                                                                                      423 GGSSGSPL 430
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29342 / M129;
05885; PubMed=8948633;
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ipoprotein MPN588 precursor (DO2_orf531)
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40, Last sequence 40, Last annotations
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521
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75.0%;
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0E706CDEC8CEEBDA CRC64;
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EMBL; AE000025; AAB55902.1; --
InterPro: IPR002414; DUF30/31.
Pfam; PF01727; DUF30; 1.
Pfam; PF01732; DUF31; 1.
                                                                                                                                                                                                                                                                                                                             004228;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Hypothetical 66.8 kDa protein in TAF40-ERV25
YML013W OR YM9571.05.
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           InterPro; IPR001012; UBX. Pfam; Pr00789; UBX; 1. SMART; SM00166; UBX; 1.
                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                 the
                                                                                                                                                                             This
                                                                                                                                                                                                 Gentles S., Bowman S., Barrell B.G., Rajandream M.A., Walsh S.V., submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Hypothetical
                                                                EMBL; Z49810; CAA89939.1; -.
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les 6; Conserv
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                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collabeen the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                              _YEAST
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tical protein; Lipoprotein; Membrane; Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation spean Bioinformatics Institute. There are no restrictions on its non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial
                                                                                                                    non-profit institutions as long and this statement is not removed.
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protein
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23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60141 MW;
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75.0%;
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Pred. No.
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N-ACYL DIGLYCERIDE (POTENTIAL).
; 0A3A089261B3C998 CRC64;
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67;
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                                                                                                                   Usage
                                                                                                                                                                                                                                                                                                                                         intergenic region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 531;
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RESULT 14
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards J., Ashburner M., Henderson S.N.,
RA George R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Burton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Wan K. H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K. H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Asbayani A., An H.-J., Andrews-pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Heimandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibeywam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibeywam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
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Matches 6
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P28668; O9VCF5;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Bifunctional aminoacyl-trna synthetase (EC 6.1.1.17) (Glutamate--trna ligase); Prolyl-trna synthetase (EC 6.1.1.15) (Proline--trna ligase); Prolyl-trna synthetase (EC 6.1.1.15) (Proline--trna ligase); AATS-GLUPRO OR CG5394.
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
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"Evolution of the aminoacyl-tRNA synthetase family and the
"Evolution of the Drosophila Plutamyl-prolyl-tRNA synthetase gene.
Intron/exon structure of the gene, control of expression of the two
mRNAs, selective advantage of the multienzyme complex.";
Eur. J. Biochem. 244:176-185(1997).
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STRAIN=Oregon-R;
MEDLINE=97217441; PubMed=9063462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aminoacyl-tRNA synthetase.";
EMBO J. 10:4267-4277(1991).
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MEDLINE=92097547; PubMed=1756734;
Cerini C., Kerjan P., Astier M., Gratecos D., Mirande M., Semeriva M.;
"A component of the multisynthetase complex is a multifunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
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NA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Sylrskas R., Tector C., Tunner R., Venter E., Wang A.H., Wang X.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
C. -(ANALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0005674; Aats-glupro.
Interpro: IPR002106; AAKRNA_ligaseII.
Interpro: IPR004046; GST_Cterm.
Interpro: IPR004046; GST_Cterm.
Interpro: IPR004526; GltX_arch.
Interpro: IPR004526; GltX_arch.
Interpro: IPR004524; Glu_tRNA-synt_1c.
Interpro: IPR004499; ProS_fam_I.
Interpro: IPR004499; ProS_fam_I.
Interpro: IPR000738; WHEP-TRS.
Interpro: IPR000738; WHEP-TRS.
Interpro: IPR001412; tRNA-synt_2b.
Interpro: IPR001412; tRNA-synt_pro.
Pfam; PF00043; GST_C; 1.
Pfam; PF00043; WHEP-TRS; 6.
Pfam; PF00587; tRNA-synt_1c; 1.
Pfam; PF00749; tRNA-synt_1c; 1.
Pfam; PF00749; tRNA-synt_1c; 1.
Pfam; PF00749; tRNA-synt_1c; 1.
Multifunctional 170 DOMAIN 755 DOMAIN 827 DOMAIN 827 DOMAIN 901 DOMAIN 980 DOMAIN 1055 DOMAIN 1129
                                                                                                                                                                           PRINTS; PR00987; TRNASYNTHGLU.
PRINTS; PR01046; TRNASYNTHPRO.
TIGREAMS; TIGR00408; pros_fam_i; 1.
TIGREAMS; TIGR00463; gltx_arch; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
PROSITE; PS00762; WHEP_TRS; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; U59923; AAC47469.1; -.
EMBL; AE003745; AAE56211.1; -.
EMBL; S18644; S18644.
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                                                                                                                                                             Aminoacyl-tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPRISED OF A BIFUNCTIONAL GLUTAMYL-PROLYL-TRNA SYNTHETASE, THE MONOSPECIFIC ISOLEUCYL, LEUCYL, GLUTAMINYL, METHIONYL, LXSYL, ARGINYL, AND ASPARTYL-TRNA SYNTHETASES AS WELL AS THREE AUXILIARY PROTEINS, P18, P48 AND P43.

SIMILARITY: IN THE N-TERMINAL LSCTION; BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diphosphate + L-glutamyl-trnà(Glu).
CATALYTIC ACTIVITY: ATP + L-proline + trna(Pro) = AMP +
diphosphate + L-prolyl-trna(Pro).
SUBUNIT: COMPONENT OF THE MULTISYNTHETASE COMPLEX WHICH IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 6 WHEP-TRS DOMAINS.
                                                                                                                                                           synthetase; Protein biosynthesis; Ligase;
  enzyme;
754
800
872
946
1025
1100
                                                                                                                                      Repeat
WHEP-TRS
WHEP-TRS
WHEP-TRS
WHEP-TRS
WHEP-TRS
                                                                                                                    GLUTAMYL-TRNA
                                                                                                                      SYNTHETASE
                                                                                                                                                             ATP-binding
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Best Local S
Matches 7
                                                                                                                                                                                                             MEDLINE-21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wingall K., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Basham D., Brown D., Chillingworth T., Fraser A., Hamlin N.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOO7_MYCLE STANDARD; PRT; 303 AA 032870; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updathypothetical protesin ML0007.
ML0007 OR MLB1770.07.
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                                               the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                           "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- SIMILARITY: STRONG, TO M.TUBERCULOSIS RV0007.
         EMBL; 270722; CAA94717.1; -
EMBL; AL583917; CAC29515.1;
                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation \cdot
                                                                                                                                                                                                     Squares S., S
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium leprae.
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TSPLP -> DKSIA (IN REF. 3).

VC -> AF (IN REF. 3).

NTACA -> KYCVR (IN REF. 3).

K -> R (IN REF. 3).

T -> S (IN REF. 3).

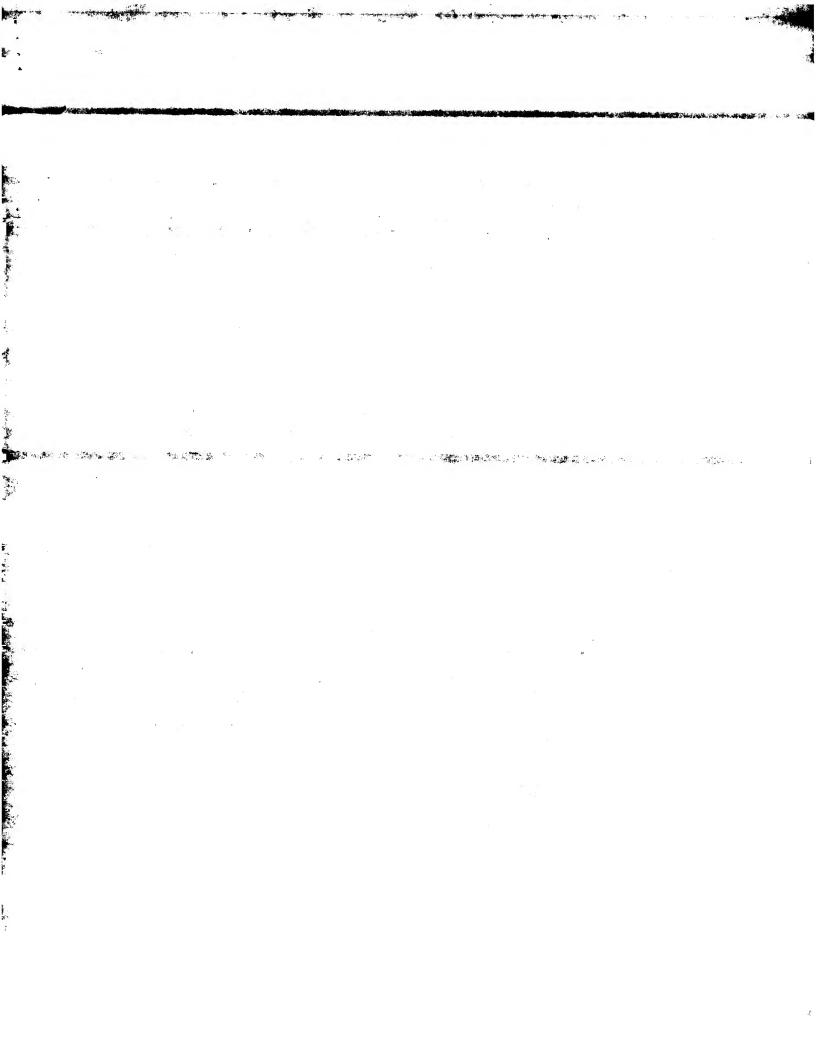
T -> S (IN REF. 3).

P -> T (IN REF. 3).

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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Command line parameters:

-MODEL=frame+_D2n.model -DEV=xlh
-Q-/cgn2_1/USPTO_spool/US10008355/runat_17122002_112703_16900/app_query.fasta_1.327
-Q-/cgn2_1/USPTO_spool/US10008355/runat_17122002_112703_16900/app_query.fasta_1.327
-DB=N_Geneseq_10102 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORME-THR_SCORE=50 -MINLEN=0 -MAXLEN=200000000
-USER=US10008355_@CGN_1_1_0_@runat_17122002_112703_16900 -NCPU=5 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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SUMMARIES

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DNA encoding novel	Japanese encephali	Human cDNA sequenc	Human full-length	Arabidopsis thalia	Human protein enco	Staphylococcus aur	Neisseria meningit	Konjak mosaic viru	Genomic sequence o	Nucleic acid seque	Bacillus lichenifo	Protease from S. A	Protease from S. A	Staphylococcus aur	Drosophila melanog	Drosophila melanog	DNA encoding novel	Ehrlichia canis im	DNA encoding Ehrli	Ehrlichia canis im	٠.	Streptococcus poly	Staphylococcus aur	Staphylococcus aur	Human ORFX ORF1506	Listeria innocua c	s enidermidis den	Staphy]ococciis eni	N. meningitiois (s	S. epidermidis ope	Arabidopsis thalia	is	Genomic sequence o	Chimeric DNA from	Yellow fever infec	DNA encoding novel	Human polynucleoti	DNA encoding novel		Human polynucleots	The Control of the Co		Porphyromonas ging	5		

7. 6.	00LT 1 .43635 AAL43635 standard; DNA; 2139 BP.	7,
	AAL43635;	,
	05-SEP-2002 (first entry)	;
	Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) coding sequence	PP-7) coding sequenc
	Dipeptidylpeptidase-7; DPP-7; gene; ds; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; gingivitis; periodontitis.	<pre>midolytic cleavage; se; gingivitis;</pre>
	Porphyromonas gingivalis.	
	Key Location/Qualifiers CDS 12139	

sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidypeptidase? (DPP-7) enzyme. The DP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide. The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a periodontal disease caused by Porphyromonas gingivalis (e.g. glupivitis or periodontitis). The present DNA sequence encodes the Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) enzyme of the invention.
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GluProGlnAspGlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLeuGluLys 80
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)B; AAO15205.
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                 The present sequence is that of the N.meningitidis strain BZ163 transferrin Tbp2 subunit gene. The Tbp2 polypeptide has three domains: an N-terminal domain, a hinge domain and a C-terminal domain; deletion mutants in which at least one of the domains is partially or totally deleted are claimed, provided that the first and second domains are not simultaneously partially or totally deleted. The positions of the 3 domains in BZ163 are defined by alignment with the IMZ169 sequence. The deletion mutant polypeptid of the invention can generate an immune response against
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                                                                                                                                                   Disclosure;
                                                                                                                                                                                      Polypeptide(s) for vaccination against Neisseria meningitidis group B - comprising deletion mutants of transferrin receptor Tbp2
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                                                                                                                                                                                                                              1996-030562/03
DB; AAR88649.
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                                                                                                                                                                                                                                                                                                       PASTEUR MERIEUX SERUMS TRANSGENE SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    meningitidis (strain BZ163).
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                                                                                                                                                 Page 82-87; 114pp; French.
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notherapy; IM2169;
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                               in BZ163 are derined by deletion mutant polypeptides
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Best Local Similarity:
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                11-JAN-2000;
02-MAY-2000;
                                               29-JUL-1999;
27-AUG-1999;
                                                                                               28-JUL-2000;
                                                                                                                              07-FEB-2001
                                                                                                                                                            EP1074617-A2
                                                                                                                                                                                                                                                      Human cDNA sequence SEQ ID NO:17412
                                                                                                                                                                                                                                                                                       26-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProGlnAspGlyAlaTrpTyrAsnTyr------HisThrThrGlyLysGly---Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAACAAGTTGGACAAAGTATGTTCCTCCAAGGC-----GAGCGCACCGATGAAAAAGAG 1665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrProGlyArgAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysSerValIleAlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAsnAlaTyrAla
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                                                                                                                                                                                                                        primer;
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 2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                               99JP-0248036
99JP-0300253
                                                                                                                                                                                                                     detection; diagnosis; antisense therapy; gene therapy;
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length CDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs. The primers allow obtaining of the full-length CDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 represent human amino acid sequences; AAB92446 to AAH3633 represent oligonucleotides, all of which are used in the exemplification of the protein second of the protein second and the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the 5002 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly t full-length cDNAs defined in the specification, and for the and/or diagnosis of the abnormality of the proteins encoded full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tull-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID 17412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes primer sets for full-length cDNAs defined in the specification.
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                             GlnLeuHisIleAlaPheLeuSerAsnAspIleThrGly-----
                                                                              GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGly---ArgTyrAlaGluAsnGly 110
                                                                                                                                                                                                                                                    GTGAAGCACCTTCCGTCTACAGAGCCTGACCCCCACGTGGTCCGTATCGGCTGGTCCCTG
                                                                                                                                                                                                                                                                                  GlyArgAlaLeuProSerAspAla----AsnPheThrMetArgMet---
                                                                                                                                                                                                                                                                                                                 AGCTATGGGGTCAGAAGGGGCCGTGTATGCTTCGAGATGAAGATCAATGAGGAAATCTCC
                                                                                                                                                        ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isogai T,
, Sugiyama
                                                                                                                                                                                                                   SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis
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T, Wakamatsu
                                                              AGCCGGTTTGAAAACTACGGAGACAAGTTTGCAGAG - -
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- AACGATGTGATTGGCTGCTTTGCGGATTTTGAA
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ı A, Nagai K
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, Otsuki T;
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                                                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAAI38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or nolynucleotide of the invention may he used to containing a polypeptide or nolynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
               in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzhelmer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome on ther uses include the utilisation of the activities such as: Immune system suppression, Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic
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Zhao
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Zhou
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Best Local Similarity:
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a control of the complementary strand of the complemen
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                   Claim
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Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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AAI61204 standard;
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US-10-008-355-2_COPY_522_712 (1-191)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity such as: Inmune system suppression, Activin/inhibin activity, Chemotactic/Chemokinetic activity haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
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19-JUL-2000;
03-AUG-2000;
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25-APR-2000;
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DB; AAM42048.
ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln
                                                  GACTCCTGCAGCACCCAGCTAGGCGAAGAGCCTTTCTCC
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The invention relates to isolated polynucleotide (I) and CC polyneptide (II) sequences. (I) is useful as hybridisation probes, CC polynerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CPC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC trestore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating CC diagnostics forensics, gene mapping, identification of mutations in CC diagnostics forensics, gene mapping, identification of mutations comes contents to assess biodiversity.
                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation diagnostics of genetic disorders or other traits and to assess
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DB; ABG27604.
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                                                                                                                                                                                                                                    RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printer specification, but was obtained in electronic format directly from W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                    02-MAR-1999
                                                                                                                                                                              AAV34396;
            EP877086-A2
                                        Synthetic.
                                                     Flavivirus
                                                                                pathogen;
                                                                                            Yellow fever virus; mutation; human; vaccine; immunity; infection;
                                                                                                                       Yellow fever infectious cDNA clone YFiv5.2/DD
                                                                                                                                                                                                         AAV34396 standard;
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                                                                                                                                                                                                                                                                                                                  CGAATCCAGAAGGAAGCCTTGGGGGGGTCAGGCCCTCTATCCTCATGTCCTGGTGAAGAAT
                                                                                                                                                                                                                                                                                                                                                                         TGTGGAAATGACGTGGAACTGTCTTTTACCAAGAATGGAAAGTGGATGGGCATTGCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnLeuHisIleAlaPheLeuSerAsnAspIleThrGly------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------AGCCGGTTTGAAAACTACGGAGACAAGTTTGCAGAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGly---ArgTyrAlaGluAsnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyArgAlaLeuProSerAspAla-----AsnPheThrMetArgMet------
                                                                                                                                                                                                                                                              TGCGCAGTGGAGTTCAACTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the Yellow Fever (YF) infectious cDNA clone YFiv5.2/DD. The sequence is derived from the YF 17D strain clone YFiv5 (Rice et al., The New Biologist 1:285-296 (1989)) by the introduction c mutations. The recombinant YF virus is useful as a human vaccine for immunity against YF infection. The recombinant YF virus vaccine is stable and safe, unlike previous vaccines which had pathogenic RNA transcripts or genetically unstable viruses which had the potential to revert back to being pathogenic, or had unacceptable neurovirulence levels when clinically tested. The new modified vaccine retains the characteristics of the current most stable and safe YF vaccine 17-DD, whilst the method for producing the virus prevents loss of immunogenicity seen with high viral passages.
                                   4994
                                                                                                    4952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10862 BP; 2966 A; 2316 C; 3083 G; 2497 T; 0 other;
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                                                                  131
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                                                                                                                                                                                                   91 GlnGluAsnIleLeuAspLeuPheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGly
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                               ATTGTTAACAGGAACGGAGAGGTGATTGGGCTGTACGGCAATGGC------ATCCTT
                                                                                                                                                                                                                                                                                                                                                                                                GlyArgAlaLeuProSerAspAlaAsnPheThrMetArgMet---SerTyrGlySerIle
SerGlyAspIleGluPheGluProAspLeuGlnArgThr 163
                                                                                                                                GlnLeuHisIleAlaPheLeuSerAsnAsnAspIleThrGlyGlyAsnSerGlySerPro 130
                                                                                                                                                                                                                                    GCTGTTCCAGGAAAGAACGTGGTCAACGTCCAGACAAAACCGAGC-------
                                                                                                                                                                                                                                                                                                       ---GGCTCATGGAAGTTGGAAGGCAGATGGGATGGAGAGGAAGAGGTCCAGTTGATCGCG
                                                                                                                                                                                                                                                                                                                                      LysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPro
                                                               ValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPheAspGlyAsnTrpGluAlaMet 150
                                                                                                                                                                                                                                                                     ---ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaVal
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                                                                                                                                                                   TTGTTCAAAGTGAGGAATGGGGGA-----GAAATCGGG
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Conservative:
Mismatches:
Indels:
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Query Match:

Best Local Percent Similarity:

Similarity:

7.76 89.50 39.22% 25.49% 8.92%

Length:
Matches:
Conservative: Mismatches: Indels:

10892 39 21 46 47

Alignment Scores

NO . .

US-10-008-355-2_COPY_522_712 (1-191) x AAF83821 (1-10892)

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                             prM-E protein deleted, truncated or mutated so that functional yellow fever virus prM-E protein is not expressed and also integrated into the genome of the yellow fever virus a nucleotide sequence encoding a prM-E protein of a second, different flavivirus so that the prM-E protein of the second flavivirus is expressed. The chimeric live, infectious, attenuated virus is used to prepare medicaments for preventing or treating flavivirus infection in a patient. The yellow fever virus vector produces its gene product (tumor antigen or cytokine) in cells of the lymphoid or reticuloendothelial system or in a precursor of these systems in patients with cancer. Flaviviruses replicate in the cytoplasm of cells so that the virus replication does not involve integration of the viral genome into the host cell. The present sequence represents a chimeric DNA derived from yellow fever virus and Japanese encephalitis virus.
 Sequence 10892 BP;
                                                                                                                                                                                                                                                            The invention relates to a chimeric live, infectious, attenuated virus comprising a yellow fever virus with the nucleotide sequence encoding
                                                                                                                                                                                                                                                                                                                                                   Chimeric live, infectious, attenuated yellow fever viruses used for preventing and treating diseases caused by flaviviruses have prM.E nucleotide sequence from a second, different flavivirus as function yellow fever prM·E is not expressed.
                                                                                                                                                                                                                                                                                                                    Disclosure; Page 200-215;
                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chambers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flavivirus febricis.
Japanese encephalitis virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yellow fever virus; prM-E protein; flavivirus; chimeric; medicament; infection; tumor antigen; cytokine; lymphoid; reticuloendothelial;
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2379 C; 3089
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RESULT 11
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         The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The
                                                                                                                                                                                                                                                                                                                                                                       Biosynthesis; biodegradation;
                                                                                                                                                                                                                                                                                                                                                                                               Genomic sequence of Lactococcus
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                                                                                                  Claim 1; SEQ ID 1; 2504pp; French.
                                                                                                                                                                                         Bolotine A,
                                                                                                                                                                                                                                            11-APR-2000;
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                                                                                                                                                                                                                                                                                                                                              Lactococcus
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                                                                                                                                                                                                                   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                              12-OCT-2001.
                                                                                                                                       New nucleotide sequence useful in
 invention
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 helps research in lactic bacteria,
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particularly useful
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Arabidopsis thaliana; thale cress; plant; transgenic; GMO; stress; metabolic pathway; biosynthetic pathway; nutrition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2365589
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Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                             Arabidopsis thaliana polynucleotide SEQ ID NO
                                                                                                                                     ABQ65948 standard;
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                                                                                                                                                                                                                           MetIleAspLysTrpGlyGln 180
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86.00
36.71%
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disease; fungicide;

371 128 311 91

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                                 US-10-008-355-2_COPY_522_712 (1-191) x
                                                                                                                                                                                                                                                                                                                                    Gorlach J, , Rameaka JG,
                                                                                                                                                                    The invention relates to nucleic acids (I) that hybridise under stringent conditions to any of 999 sequences (ABO65424-ABO66422) or their fragments. (I) are used to express the corresponding polypeptides (II) or to produce genetically modified plant cells or transgenic plants, which may have improved resistance to disease or stress, or altered metabolic/blosynthetic pathways (for production of commercial, nutritional or medicinal products), or generally any trait of interest, or can be used to screen for biologically active agents (e.g. fungicides,
                                                                                                                                      Insecticides and antibiotics).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO at segdata.uspto.gov/sequence.html?DocID=999909770149.
                                                                                                                                                                                                                                                                   New nucleic acid that hybridizes to A useful e.g. for preparing transgenic or altered metabolism -
                                                                                                                                                                                                                                                                                                                      Garcia CA,
Hurban P;
                                                                                                                       Sequence
                                                                                                                                                                                                                                                    Claim 1;
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(LEDF/)
(WOES/)
(HAAS/)
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                                                                                                      Scores:
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LEDFORD B L.
WOESSNER J P.
HAAS W D.
GARCIA C A.
KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
ALLEN K.
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HOFFMAN N.
HURBAN P.
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RAINES T M.
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                                                                                                                     651 BP; 185 A; 110
                                                                                                                                                                                                                                                   SEQ ID NO 525;
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Kricker M
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T, Davis KR,
                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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Allen K,
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JP, Haa
Hoffman
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RESULT 13
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ID AAC46
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06-MAY-1999;
07-MAY-1999;
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30-APR-1999;
04-MAY-1999;
05-MAY-1999;
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16-APR-1999;
19-APR-1999;
21-APR-1999;
23-APR-1999;
23-APR-1999;
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
                                                                                                                                                                                                                                                                                                            05-MAR-1999
09-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
                                                                                                                                                                                                                                                                                                                                              25-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGCCATTGCTTGATTCTTATGGCCATACCATAGGTGTGAACACTGCCACATTCACCCGA 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGAAGAGTATTTCAGAAGCTATACAAACCGATGCTGATATTAACTCAGGCAATTCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyGln----LeuHisIleAlaPheLeuSerAsnAsnAspIleThrGlyGlyAsnSerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAAACACCTTGACAATAGGGGTAGTAAGTGGGTTGGGAAGAGAGATACCTTCACCTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATCTAGCTGTGTTGAAGATTGAAACTGAGGGACGTGAACTAAATCCTGTTGTTCTCGGT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGGGAGTGGTATGTCTTCTGGTGTTAACTTT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThrIleSer 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCTCCAATGATCTACGCGTAGGTCAAAGTTGCTTTGCGATTGGGAATCCATATGGATAT 251
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990S-0126264

990S-012785

990S-0127462

990S-0128734

990S-0128714

990S-0130077

990S-0130091

990S-0130091

990S-0132449

990S-0132487

990S-0132484

990S-0132485

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990S-0132485
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RESULT 14
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26-OCT-1999
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28-OCT-1999
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28-OCT-1999
17-MAY-2001
                     WO200134809-A2
                                                               Staphylococcus epidermidis vaccination; endocarditis;
                                                                                                S. epidermidis
                                                                                                                       03-SEP-2001
                                                                                                                                             AAH53441;
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                                         Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGCTAAGGGAACAAGATTTAGCAAGGAAGGGAAAAATTGTGGGTCTTGATCCAGATAAT 561
                                                                                                                                                                                                            ATTGACACAGTTGTCCGAACAGTTCCGTACCTCATT
                                                                                                                                                                                                                                Valasp-----IleargTyrValLeuPheMetIle 175
                                                                                                                                                                                                                                                                                                 GGGCCATTGCTTGATTCTTATGGCCATACCATAGGTGTGAACACTGCCACATTCACCCGA
                                                                                                                                                                                                                                                                                                                                                                  GlyGln---LeuHisIleAlaPheLeuSerAsnAsnAspIleThrGlyGlyAsnSerGly
                                                                                                                                                                                                                                                                                                                                                                                        ValLeuGluLysGlnAspProLysSerAspGluPheAlaVal----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATCTAGCTGTGTTGAAGATTGAAACTGAGGGACGTGAACTAAATCCTGTTGTTCTCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scores:
                                                                                                                                                                                                                                                        AAAGGGAGTGGTATGTCTTCTGGTGTTAACTTT----
                                                                                                                                                                                                                                                                            AsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThrIleSer
                                                                                                                                                                                                                                                                                                                      SerProValPheAspLysAsnGlyArgLeuIleGlyLeu-----AlaPheAspGly
                                                                                                                                                                                                                                                                                                                                             GGGAAGAGTATTTCAGAAGCTATACAAACCGATGCTGATATTAACTCAGGCAATTCTGGA
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                                                                                                                       (first
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99US-0161359.
99US-0161360.
99US-0161361.
99US-0161920.
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99US-0161993.
99US-0162142.
                                         epidermidis
                                                                                              open reading
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99US-0161405
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99US-0160989
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85.50
38.16%
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                                                                                                                                                                  606
                                                                SR1
                                                                                                frame nucleotide sequence SEQ ID
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                                                                          strain;
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                                                                          infection; diagnosis
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42
16
67
27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (1) and (II) can have antibacterial activity and therefore can be used (I) and (II) can have antibacterial activity and therefore can be used (I) waccination. The nucleic acids (I) may be used to produce the CC s. epidermidis polypeptides (II) via the production of vectors (CC containing them which are used to produce hosts cells which express the CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AhH53971 to CC AhH55090 represent specifically claimed S. epidermidis genomic DNA (CC polypucleotide sequences from the present invention. AhH55091 to AhH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

CC N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4456 to 4472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 605-606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH52304 to AAH53970 represent nucleic acids (I) encoding (II), given in AAG81454 to AAG83120, from Staphylococcus (I) and (II) can have antibacterial activity and therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for vaccinating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-316495/33.
P-PSDB; AAG82591.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       no sequences are present for SEQ ID NO:4455 to 4464.
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292
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                                                                                                                                                                                                                                                                                                                                                                                                                   IleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThrThrGlyLysGly 76
AAAAAAGAATCT----GTTGAGGATACTGCTAAAGTTTTAGGCAGAATGTTTGATGGA
                                                                           GCATCTATTGATCTAGGTGCACACCCTGAATTTTTAGGGAAAAATGATATTCAATTAGGA
                                                                                                                                                    AAGAATATTGCTTTACTCTTCGAAAAGACATCTACTCGGACGCGTGCCGCATTTACAGTT 231
                                                                                                                                                                                      GlyGlnLeu-----
                                                                                                                                                                                                                               TTTGCTATGACATTAAAAAATATAAACAACAAGGCACACCACATCGATATTTAGAGGGT 171
                                                                                                                                                                                                                                                                                                       TTGCTAAAAGAGTATGATCTTACAGGTGAAGAATTT-----GAAGGTCTAATCGAT
                                                                                                                                                                                                                                                                                                                                            ValLeuGluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAsp
                                   AsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPheAspGly
                                                                                                                                                                                                                                                                 LeuPheArgThr---LysAsnTyr------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides from Staphylococcus epidermidis,
against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2188pp; English
                                                                                                              -HisIleAlaPheLeuSerAsnAsnAspIleThrGlyGly 125
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                 -GlyArgTyrAlaGluAsn 109
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46
46
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RESULT 15
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                        CC (bleb) preparation from a Gram-negative bacterium for use as a vaccine.

CC The blebs of the invention are improved with respect to their considerable of the invention are improved with respect to their considerable of the blebs of the invention are improved with respect to their considerable of the blebs are considerable of the changes to the chromosome of the bacterium from which the blebs are considerable of the changes made include the upregulation of protective antigen considerable of the changes made include the upregulation of protective antigen considerable of the changes which result in detoxification of the chormasses modified Gram-negative bacterial strains from which the bleb considerations are made, a vector suitable for performing recombination consideration of the modified bacterial strains), in the devents (for the generation of the modified bacterial strains), considerable for performing recombination and immunoprotective and non-toxic Gram-negative bleb phost, or killed whole colling the manufacture of a medicament for immunising a human host against a considerable of the influenza virus. Bacterially derived nucleotide sequences of the invention are used in the performance of homologous recombination events up to 1000 by upstream of a bacterial chromosomal gene in order to either increase or decrease expression of that gene. Immunoprotective and concrease or decrease expression of that gene. Immunoprotective and concrease of the present sequence represents a specifically useful colaimed Neisseria meningitidis nucleic acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 46; Page 81; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    microbial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide useful for outer membrane vesicle preparation from Gram-negative bacterial strain for vaccination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetically modified; protective antigen expression; LPS detoxification;
LPS; lipid A; homologous recombination vector; immunisation;
immunoprotective; non-toxic; paediatric; cyclic; circular; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified Gram-negative bacterium; outer membrane vesicle;
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Best Local Similarity:
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                           ProAspLeuGlnArgThrIleSerValAspIleArgTyrVal 171
                                                                                       LeuIleGlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGlu
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                                                                                                                                                                                                                                                                                                                                    ProGlnAspGlyAlaTrpTyrAsnTyrHisThrThrGlyLys------GlyVal 77
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                                                          ATTGAGGGCAACGGTTTTTCCGGTACG-----GCGAAAACTGCTGACTCAGGTTTTGAT
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Search completed: December 21, Job time: 749 secs 2002, 02:00:26

Sequence

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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-O-/cgn2_1/USPTO_spool/US10008355/runat_17122002_112704_16920/app_query.fasta_1.327
-OB-GenEmbl -QFMT-fastap -SUFFIX-p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXY=0
-UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45
-OCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEADSIZE-500 -MILEN=0 -MAXIEN=2000000000

-USER=US10008355_@CGN_1_1_1616_@runat_17122002_112704_16920 -NCPU=6 -TCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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37: em_htg_vrt:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RS Simpson, A.J.G., Reinach, F.C., Arruda, P., Abreu, F.A., Acencio, M., Alvarenga, R., Alves, L.M.C., Araya, J.E., Baia, G.S., Baptista, C.S., Barros, M.H., Bonaccorsi, E.D., Bordin, S., Bove, J.M., Briones, M.R.S., Bueno, M.R.P., Camargo, A.A., Camargo, L.E.A., Carraro, D.M., Costa, M.C., Franco, M.C., Goldman, M.H.S., Comes, S.L., Gruber, A., Ho, P.L., Hoheisel, J.D., Junqueira, M.L., Kemper, E.L., Laigret, F., Lambais, M.R., Kitagian, J.P., Krieger, J.E., Kuramae, E.E., Laigret, F., Lambais, M.R., Machado, J.A., Machado, M.A., Machado, M.A., Machado, M.A., Machado, M.A., Machado, M.A., Machado, M.A., Matrins, E.A., L., Marques, M.V., Martins, E.A., L., Marques, M.V., Martins, E.A., L., Martins, M.C., de Oliveira, M.G., de Oliveira, M.G., Martins, E.A., L., Martins, E.A., Moon, D.H., Nagai, M.A., Peixord, M.A., Moon, D.H., Nagai, M.A., Martins, E.A., L., Martins, E.A., L., Martins, E.A., L., Martins, E.A., L., Martins, E.A., Moon, D.H., Nagai, M.A., Persun, M.A., Moon, D.H., Nagai, M.A., Martins, M.A., Martins, M.A., Martins, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The genome sequence of the plant pathogen Xylella fastidiosa. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing and Analysis
Nature 406 (6792), 151-157 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-2000) Organization for Nucleotide Sequencing and Analysis, Bioinformatics Lab - IC/Unicamp, C.P. 6176, Campinas, SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xylella fastidiosa 9a5c,
AE004008 AE003849
AE004008.1 GI:9106961
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Xylella fastidiosa 9a5c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submission
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similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                             complement(119 .367)
/gene="XF1871"
                                                                                                                                                                         complement(119. .367)
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/clone="9a5c"
                                                                                                                                                                                                                                                                                                                                                                                                                             1. .10689
/product="hypothetical protein"
                                                                    /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Xylella fastidiosa 9a5c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brazil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1839.
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similarity; putative; ORF located using Glimmer/RBSfinder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mTmTlKeDKTEIIDEQRIQIAKLLSETAKIQAEIHEVNAHTQKL
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/txanslatjon="MYMTLKEDKTEIIDEQKYSYEVVVVASGLLAAGATAATLFIKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLIQRQQKRKASP"
1351. .1662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mSKnKipnQiltGnwagfQfingKlvTperrtieewQlrwlsLtCTLAREwQKmweeAratapQgglaasDpQritDalQKTvSHKrrhaanetasiiQlrQ
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similarity; putative; ORF located using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(430. .618)
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Glimmer/RBSfinder"
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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                   US-10-008-355-2_COPY_522_712 (1-191) x AE004008 (1-10689)
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                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                        Alignment
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                                                                                         GCGCGTCCGATCTACTTGCAAGCCTTAGCTGAC---TACAACAAGAGTCATGGCAAA--- 8811
                                                                                                                                AlaArgAlaIleGlnAlaAspAlaMetAlaAsnAlaTyrAlaIleGluLysGlyLysArg
                                           LeuPhePheAlaGlyLeuArgGluMetTyrProGlyArgAlaLeuProSerAspAlaAsn 47
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complement(4481. .4702)
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similarity; putative; ORF located using Glimmer/RBSfinder"
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AYIAGGFRGVKNV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVILDTDLGQLVRSDPSTVNAVLTDSQTGAVLLTPEIVSALNKLRRSLEDELKASHAP
DQQPSSGGASSPPSSSGTAWPSFCSWASVVCDFIDWVKSDEFLKKPLVPPDVPYVDKL
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="XF1879"
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/protein_id="AAF84684.1"
/db_xref="GI:9106969"
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similarity; putative; ORF located using
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThrIleSer 165
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Consensus quality: 207648 bases at least Q40 Consensus quality: 225569 bases at least Q30 Consensus quality: 225569 bases at least Q30 Estimated insert size: 250510; agarose-fp estimation Estimated insert size: 249417; sum-of-contigs estimation Quality coverage: 9.03 in Q20 bases; agarose-fp estimation Quality coverage: 9.07 in Q20 bases; sum-of-contigs estimation.*
* NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                         Submitted (04-DEC-1999) Production Sequencing Facility, D
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9
On Apr 20, 2001 this sequence version replaced gi:7711568
                                                                                                                                                                                               Project Information
Center Project Name: 940643, BC905667
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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                                                                                                                                                 Summary Statistics
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consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Caps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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1: gap of unknown length
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                                                                                                                                                                                       TGANACACGTCGACCACGCAGACAACCTGCTGAAAGAAATG 4263
                                                                                                                                                                                                        uPheGluPro-AspLeuGlnArgThrIleSerValAspIleArgTyrValLeuPheMetI 175
                                                                                                                                                                                                                                                                                                                         AGGCGAATTCATCGGCCTGGCGTTCGACGGCACCCTGGACTCGATCATTTCCGACTGGGA 4364
                                                                                                                                                                                                                                                                                                                                           nGlyArgLeuIleGlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIleG1 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAATGGCCTAAGGACTTCGGCAAATTTGTCGATCCGAAGCTGAAAACCGTGCCGGTCGA 4484
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                                                                                                                                                                                                                                                         CTACAACAAGGCCGAACACCCGTTCGATCCAGGTCGACCTGCGCTACATGCTGTGGAACA 4304
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Xanthomonas axonopodis
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/db_xref="taxon:9606"
/chromosome="19"
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,49: gap of unknown ...
,435: contig of 19303 bp in ...
64452: gap of unknown length
170540: contig of 6088 bp in length
185046: contig of 14406 bp in length
185146: gap of unknown length
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222209: contig of 37063 bp in lengt
222309: gap of unknown length
222309: gap of unknown length
222317: contig of 30908 bp in length
757217: contig of 30908 bp in length
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Chambergo, F., Ciapina, L.P., Cicarelli, R.M.B.B., Coutinho, L.L.,
Cursino-Santos, J.R., ElDorry, H., Faria, J.B., Ferreira, A.J.S.,
Erreira, R.C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C.,
Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite
Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A.,
Martinez-Rossi, N.M., Martins, E.C., Meddanis, J.,
Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M.,
Menck, V.K., Oliveira, M.C., Oliveira, V.R., Pereira Jr., H.A.,
Rossi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F.,
Takita, M.A., Tamura, R.E., Teixeira, E.C., Tezza, R.I.D., Trindade dos
Santos, M., Truffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cursino Santos, J.R., El Dorry, H., Faria, J.B., Ferreira, A.J.S., Ferreira, R.C.C., Ferro, M.I.T., Formighieri, E.F., Franco, M.C., Greggio, C.C., Gruber, A., Katsuyama, A.M., Kishi, L.T., Leite Jr.R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A., Madeira, A.M.B.N., Martinez-Rossi, N.M., Martins, E.C., Meidanis, J., Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Moreira, L.M., Novo, M.T.M., Okura, V.K., Oliveira, W.R., Pereira Jr., H.A., Rossi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Sphoola, L.A.F., Takita, M.A., Tamura, R.E., Teixeira, E.C., Tezza, R.I.D., Trindade dos Santos, M., Tuffi, D., Tsai, S.M., White, F.F., Setubal, J.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kitajima,J.P.
Comparison of the genomes of two Xanthomonas pathogens with differing host specificities
Nature 417 (6887), 459-463 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (28-NOV-2001) Departmento de Bioquimica, Universidade Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R., Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertolini,M.C.,
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                                           complement(1840.
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                                                                                                                                                                                                                                   DVIGEDVLITGAGPIGIIAAGICKHIGARNVVVTDVNDFRLKLAADMGATRVVNVSKT
                                                                                                                                                                                                                                                                       RPHLCPNTVGIGVNVNGAFAEYMVMPASNLWPIPDQIPSELAAFFDPYGNAAHCALEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
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6791..705/
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VFDFRKPDDSALSALPSVDDYRARTAAVRDKPLPSAPAAATMPRQEPGQRPARALPYA
LQVHARVQEGAAVQLQEVNSGAAAAAENVYNSAAGGGPWYYTVLPGTQLDDAPTGATH
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LNYGAKALSTTTRAQSLVPTTALAQGRIRAEDNFLPQLGINYKLDERQDLYASYSKNI
AAFGFTPFATSQAAFDRSRSTLEPEQSQTVQVGYRVQDAQFQLSADAYFTKFSNRLLT
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QWGDGNRLSLFVDTSRRKEYDYMDLSLTSQRALGWNYDYLQPDMATAVQWARAYQNYR
QWGDGNRSLFDYSKLDASYYAGGGLRDDNLAGLSGTFVFGGATLDAGSY
ATSGVANGYPQSLAGLFSDYSWLDASYYAGGLRRDNLAGLSGTFVFGGATLDAGSY
HGNRGEGQWVTPYVRTSAQIPVSMRTTDYGLDRFGGTSALKWSWGNHDLEVGAWAENA
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QDIEQLTPGSSAFKAVEKLPGVQFQSADPFGTYEWSTQVTLHGFDQSRLGYTLDGIPL
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LRALDYADPSARTLSLAAGQRETIRLALAASDHWYDLVVEQPGSAFRRRLAGHLETGR
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located using Blastx/Glimmer/Genemark"
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                                                                                                                                                                                                                                                                                                                    GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPheAsp 144
          TTGAAGGAACTC 7224
                                                                                          GCCGTGGACGGCCGCTATCTGCGTTGGATCATGACCGAGGTCGCTCCGGCGCCACAGCTG
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                                                                                                                                                 SerValAspIleArgTyrValLeuPheMetIleAspLysTrpGlyGlnCysProArgLeu 184
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located using Blastx/Glimmer/Genemark"
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located using Blastx/Glimmer/Genemark"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
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50.00%
17.45%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches: Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
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REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
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KEYWORDS
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
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Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biologie Moleculaire des Interactions Plantes-Microorganismes INRA-CNRS, BP27, 31326 Castanet-Tolosan Cedex, France, Fondation Jean Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France, LMGM CNRS 118 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA URGV, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biometrie et Intelligence Artificielle INRA, BP27, F31326 Castanet-Tolosan Cedex. Laboratoire de Genetique Cellulaire INRA, BP27, F31326 Castanet-Tolosan Cedex Christian, Boucher@toulouse.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salanoubat, M., Genin, S., Artiguenave, F., Gouzy, J., Mangenot, S., Arlat, M., Billault, A., Brottier, P., Camus, J.C., Cattolico, L., Chandler, M., Choisne, N., Claudel Renard, C., Cunnac, S., Demange, N., Gaspin, C., Lavie, M., Moisan, A., Robert, C., Saurin, M., Schiex, T., Siguier, P., Thebault, P., Whalen, M., Wincker, P., Levy, M., Weissenbach, J. and Boucher, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ralstonia solanacearum.
Ralstonia solanacearum
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     segment 17/19.
AL646073 AL646052
AL646073.1 GI:17429991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 204050)
Boucher, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished 2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ralstonia solanacearum GMI1000 chromosome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://sequence.toulouse.inra.fr/R.solanacearum.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome sequence of the plant pathogen Ralstonia solanacearum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ralstonia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /function="small molecule metabolism; central intermediary metabolism; nucleotide hydrolysis"
complement(1298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(115. .1278)
/gene="dgt"
                                                                           complement(1298.
                                                                                                                                                                                                                                                                                                                    /product="PROBABLE DEOXYGUANOSINE TRIPHOSPHATE TRIPHOSPHOHYDROLASE PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(115.
                         /note="RSc2969;
                                                                                               LFRVFLEDPRLLPPQYQARDPADQPRWIAHYIAGMTDRYAIKEHRRIFAVEVL'
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  RS01328"
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                                                                           2404)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3114. .5258)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVPVIFEHEGEMGFRDRETQMIDELTARHGVVVVATGGGAVLRPENRAFLRERGTVIYL RANPHDLYLRTRHDKNRPLLQTENPRARLEELHAIRDPLYREVAHFVIETGKPTVAQL VNMVLMQLEVAGIVVPPAASSPTSQVSRQS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biosynthesis; chorismate"
/note="Product confidence : prol
Gene name confidence : probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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Gene name confidence : probable
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                                                                                                  FAAPAPTAGVERPSVRNIDFRRGEELAGRVVVDLSTSNSAINIAQQGQNLVVDFAGAT
LPQSLRRRFDVSDFGTPVQAMRATDNGTGARLVIEPRGNWQYSSYQTDTQFVVEVRPT
KEDPNKLISGPGYRGERMSLNFQNIDIRSLLQVFADFTNLNIVTSDSVTGTLSLRLKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                            predicted by Codon_usage
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="structural elements; cell exterior; surface
structures"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(3114. .5258)
/gene="pilQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             predicted by Codon_usage predicted by Homology predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2401. .2973)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKLGQAFVTTVPDTDLRATLQHAVLRPPTEAPVA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRGSVQIKAAVVAQDERESGLRAILNFGHTFGHAIEAGLGYGEWLHGEAVGCGMAMAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLSHRLGFIDIDTRNRVTALTRAANLPVVAPDLGVARFIDLMRVDKKAEAGEIKEVLL
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KDATWDNSAAVSLPANGINGVNAASVAVSLFNAGAGRFLALELSALEADGRGKIISSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Product confidence :
Gene name confidence : prob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="RSc2971; RS01326"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /EC_number="4.6.1.3"
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                                                                                                                                                                                                                                                                                                                                                    /product="PROBABLE FIMBRIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable
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                                                                                                                                                                                                                                                                                                                        Percent Similarity:
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                      36
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CDS

gene

gene

CDS

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Db 190879 ATCACCAACTGCCACGTGCTGCGCGGCGGCAAGCAGGTCTGGCTCAAG----
                                                                                                                                                                          US-10-008-355-2_COPY_522_712 (1-191) x AL646073 (1-204050)
                                                                                                                                                                                                                                                                             Best Local Similarity:
MetAlaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGlu 35
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predicted by Codon_usage
predicted by FrameD"
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complement(5797. .6462)
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complement(5255. .5800)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNLFKSTAKTNDRTELLVFLTPRVLSDQLSLK"
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NKDSLGTQTTNGFAINTKHVQTQVLVENGGTVVIGGIYTQNERTDVNKVPLLGDIPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             structures"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(6459.
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/gene="pil0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="PROBABLE FIMBRIAL TYPE-4 ASSEMBLY LIPOPROTEIN"
/protein_id="CAD16681.1"
/db_xref="GI:17429996"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           structures"
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                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Product confidence : probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="pilN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="RSc2974; RS01323"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="pilN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product="PROBABLE FIMBRIAL TYPE-4 ASSEMBLY MEMBRANE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'function="structural elements;
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24.09%
10.12%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerAspGluPheAlaValGluGluAsnIleLeuAspLeuPheArgThrLysAsnTyrGly 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nolling,J., Breton,G., Omelchenko,M.V., Markarova,K.S., Zeng,Q., Gibson,R., Lee,H.M., Dubois,J., Qiu,D., Hitti,J., Wolf,Y.I., Tatusov,R.L., Sabathe,F., Doucette-Stamm,L., Soucaille,P., Daly,M.J., Bennett,G.N., Koonin,E.V. and Smith,D.R. Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum
J. Bacteriol. 183 (16), 4823-4838 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-JUL-2001) GTC Sequencing Center Production, Finishing, and Bioinformatics teams, Genome Therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Childress, D., Zeng, Q. and Smith, D.R.
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Clostridium acetobutylicum
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Clostridium acetobutylicum ATCC824
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                                                                                                                                                               /transi_table=11
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/db_xref="GI:15023528"
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FERKELRARLAALIRRNYNRPSNEIKIKDLANIDTKAKSYKVGEKLITLTAREXYDIEL
LCYNYPNIVSAEEIIEHVWGDNDNQFSNVIRVHIANLRRKIKCSGGETLIETLKGKGY
  /gene="CAC0654"
                                                                                                                                                                                                                                                                                                              /gene="CAC0653"
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154. .819
                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Clostridium acetobutylicum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:1488"
                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="ATCC:824"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:15023527
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YTFVWKKVIYKNEGKKKFLIALVEDINLENLKGFTIGKETLIDDINKILQWLLFEKE
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KKDDHMRNGQLKPAYNVQIAVDSEYVTGVGVFDDRNDIATLIPMITNMQKKLVIHTPM
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GVIDVYKTEKGRYQNKYTGNYLETIFNNGKVIISTILEDDYSEDNLSKCYGTKKIKYY
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/db_xref="GI:15023533"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="CAC0657"
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/db_xref="GI:15023532"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="CAC0657"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MFLESNNQIPYIKPQTYEKWKKRSFKNDISRRENMEYDAKTDTYTCHNNRKLSPSCIIHKKSASGYTSEVTVYECEICDNCTLKPKCTKAKKNRKMQVSKAFIKKREISYNNIKTELGTKLRWNRSIQVEGAFGVLKSDYEFKRFLTRGKNSVKTEFILL
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/gene="CAC0656"
PKGCEKNYGMELIQWSESKYKSELKSDGKIDMFNEEFVVHPILRIHGRRISAKSESG)
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/transl_table=11
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/protein_id="AAK78633.1"
/db_xref="GI:15023531"
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/protein_id="AAK78632.
/db_xref="GI:15023530"
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/db_xref="GI:15023529"
/translation="MLKIKSRIALLYSMLTIALIIIFIISFCLILNIYINKRPILDSI
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/transl_table=11
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/gene="CAC0659"
/codon_start=1
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NGIIVPINMVISKYLIDSVVNALKNKSGSFLSSKNIIKTVKLLWKSSSLSFIATLIITVL
NGIIVPINMVISKYLIDSVVNALKNKSFIDSFYNKIEKANSQAVGTTIQIVNGLTO
FSTIQSKCLINISISELLIKKANELDLSYFENDEFYNKIEKANSQAVGTTIQIVNGLTO
IVKNETTLVGAIVIVEQLSFIILLLCIMTSIPMFIINIKIYKQKKNIYSKRIEKTRLA
HYLQAVMMDYIPVKEIKURIGDWLEKIILSIYKDULNQDKKLEKQLLIMSIVDIFN
TIISYGYKIVLIFTILTGCNLSKISHNYISATINLDDSVKNYTLDNFALLYSNILYIEN
TIISYGYKIVLIFTILTGCNLSKISHNYISATINLDDSVKNYTLDNFALLYSNILYIEN
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GINENDFVKYKRIFYKDLKSYHKEYKYYQSEEIIKECINNFLYDEELMTLSNEYEACN
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GOWQKLAISRAFMSNACLLILDEPTASIDAKSEYELFKDFKELMGEGTSILISHRFST
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/protein_id="AAK78638.1"
/db_xref="GI:15023536"
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9167. | 9370
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lmeqglþngtahftehlcidsnvaylknygkyyednnilggytmepgtyyyfoctidn
idegesýfknilsdoetidrrlmekkkdliveldyrmkgangglqnnilpvilgdkni
kdkfplýkikciekmefqsvksfhdkwykpqnsaicicgdiansdienkiskyfsefk
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/protein_id="AAK78636.1"
/db_xref="GI:15023534"
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9575. .11458
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/protein_id="AAK78637.1"
/db_xref="GI:15023535"
/translation="MKLVNPVGRDLTELETEAYSCHCICSSGSYTAKNRGYHGGYDAC
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KDCSRCWAARLCNVCYSHCYTDGKLDMKEKKRYCIRSRERALRSLVFYHKCAEINPEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATAAGGGATTTAAAATGACATCAGGAGAATTTGAAGCTGCGGTAATGCATGTACTCTAT 1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATAAGAATCCAGAAAATTGATGATAGTGTTTATGATAAAATGTTTTGGTGAACTTTCAAAT 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAATAATATGAGTGGT-----AAACTATCTATAGTAACAGATAAGAATGATAGCGTA 1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTACTAAAAATTTA---AAGTATTATTCTAAAGGCCAGATTTTCATTAAGGATTTACTT 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGAGATTTATTATATTATATTATAATT 1529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValAspIleArgTyrValLeuPheMetIle 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleGlyLeu----AlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIle-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AsnAsnAspIleThrGlyGlyAsnSerGlySerProValPheAspLysAsnGlyArgLeu 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHisIleAlaPheLeuSer 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTACTATACTTCCA - - - - - GATGATTATTCA - - - GAGGATAATCTGAGTAAGTGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isopentenyl-diphosphate delta-isomerase;
ATP-dependent RNA helicase.
Aspergillus fumigatus.
Aspergillus fumigatus
Eukaryota; Fungi; Ascomycota; Pezizomyco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79718 bp
Aspergillus fumigatus BAC AFA12F2.
AL807577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eurotiales; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus. 1 (bases 1 to 79718)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harris, D.E., O'Neil, S., Knowl Woodward, J.R., Denning, D.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL807577.1 GI:21627806
3-hydroxyisobutyrate dehydrogenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (24-JUN-2002) The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xxef="taxon:5085"
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/gene="AfA12H2.01"
join(2. 1327,1382. .4864)
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/note="Similar to Saccharomyces cerevisiae hypothetical
/note="Similar to Saccharomyces cerevisiae hypothetical
26.9 9 kDa protein in fkh1-metl8 intergenic region yill29C
SW:YIM9_YEAST (P40468) (2376 aa) fasta scores: E():
2.1e-67, 32.42% id in 1496 aa
Signal peptide predicted for yill29C by SignalP 2.0 HMM
(Signal peptide probabilty 0.606, signal anchor
probability 0.000) with cleavage site probability 0.431
between residues 18 and 19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Aspergillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Knowles,D.G., Hall,N.,
D.W., Anderson,M.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fumigatus"
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Barrell, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLN
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GIEDBYWSI RRSDPKVVWEY EDNNOKEDGDOGSRVPLSMSTVTRQVVNFSSAYEGVS
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SANYLGDEFEDGLYEEDGERLTNNKP.PFYFHNGSGRSVTDGSSSIESMIRSGMRRLTGG
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/note="Similar to Schizosaccharomyces pombe hypothetical force" Similar to Schizosaccharomyces pombe hypothetical 62.9 kDa protein c29a10.02 in chromosome ii spbc29a10.02 or spbc365.18 TR:094381 (EMBL:AL034463) (567 aa) fasta scores: E(): 3.1e-05, 33.85% id in 319 aa pfam:PF00076;RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain);0.16;codon 51-119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLISLPDSKSRNSRLKDLEDKTSTNIYCTNVPITWTEADLRHHFEPYHVVSEKISRDE
KTGVSKEVGFARFDTREIAEKVLGEFHNISKNGVKLLLRFADTKAQKMLKQQSNERRA
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/translation="MKTPNGYMLQdlesitqqeppipravpam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prosite pattern:PS50102;Eukaryotic RNA Recognition Motif
(RRM) profile:;10.326;codon 126-203"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STGRCWPMEVNNPVPGVVETAPASRGYEGGFGVGLMKKDLRLAITAAKESGTPLALAE
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join(9141...9470,9608...9697,9745...9839,9901...10219,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTMKVEVAQSAREVAEQSTVMITSLPEPEHVKDVFHSILKHGDLPALEEERLFIDTST
IDPASSKEIANAIHSTRTGHFVDAPMSGGVVGARAGTLSFMFGASSQSGGLIERVRAV
LMLMGKKAWHLGPPGAGVSGKLANNYILAINNIATAEAMNLGTRWGLDPKSLADMINT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative 3-hydroxyisobutyrate dehydrogenase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVVPKNMVQERKDITPAPPDVKSLPYVADLGTVLPVGNKQAGLSLGQVALIFLVDLMV
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                                                          complement(join(11060. 12210. .12266))
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10233. .10567)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATWGFIGLGQMGYLMAKNLRAKIPATDTLLVRDVNENATTRFVEETKEAAKSSGAAD
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                                                                                                                                                                                /gene="AfA12H2.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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/gene="AfA12H2.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                                                                                                                            .11087,11156.
                                                                                                                            .11243,11312.
                                                                                                                            .12053
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domain;3.6e-27;codon 305-388
prosite profile:PS00039;DEAD-box subfamily ATP-dependent helicases signature Confirmed by InterPro eMOTIF pattern match;8e-5;codon 198-206"
                                                                                                                                      GHLPKERQTILLFSATQTKKVSDLARLSLQDPEYVÄVHETASSATPSKLQQHYVITPLP
QKLDILMSFIRSNLKSKTMVFLSSGKQVRFVYESFRHLQPGIPLMHLHGRQKQGGRLD
IVTRFSQSKHCVLFSTDVAARGLDFPAYDMVIQLDCEBDADTY HRVGRTAR VEREGR
AVLFLDPSEEEGMLKRLEQKKVPIEKINIKANKQQSIKDQLQNMCFKDPELKYLGQKA
FISYVKSVYIQKDKEHFKLKELKLDEFAASLGLPGAPRIKFIKGDDTKQRKNAPRAAA
HLLSDDDDTDEEDGEKKSKKKEEEPQVRTKYDRMFERRNQDVLAEHYSKLINDDGTMDL
GSSGDEDDESEKGNKKNVKVRREKLLKSKKKLLKFKGKGTKLVYDDEGNPHELYELED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Similar to Schizosaccharomyces pombe probable fad synthetase spcc1235.04C SN:FAD1_SCHPO (074841) (265 aa) fasta scores: E(): 7e-31, 40.61% id in 261 aa pfam:PF01507;Phosphoadenosine phosphosulfate reductase family:1.8e-11;codon 62-249"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Similar to Schizosaccharomyces pombe probable ATP-dependent RNA helicase spac1093.05 TR:Q9UTP9 (EMBL:ALI32839) (735 aa) fasta scores: E(): 1.5e-118, 53.67% id in 749 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Similar to Schizosaccharomyces pombe DNA j domain containing protein spbcl734.05C TR:074746 (EMBL:ALO31856) (209 aa) fasta scores: E(): 2.1e-17, 41.62% id in 185 aa prosite pattern:PS50076;dnaJ domain profile.;11.351;codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTSDTHPNPKLRVEHSADPGOGVADGTOSQHYRPAYELTEDQEERLGRILNNPFSISQ
SSSLTSFYHSFAPQTPDVGRCSNATELD"
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SLNVIATALSRYKLSELSLSYNGGKDCLVLLILFLASLHPHPPPEEGGLAYIRAI
PPDSSPAVEEEVQNGSRAYHLAIVRETTEPPRTTLKSCFEHYLSLNPSIKAIFVGTR
TDPHGANLTHFDPTDSGWPDFMRIHPVIDWHYAEIWAFIRHLGLKYCSLYDRGYTSLG
                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mapaagprtgkhakpqrsktlkrkrgqeelssliqrvedldlkg
Ifksfsdlplseptasglasshyktltdiqsraishalkgrbilgaaktgsgktlafl
VPVLENLYRRQMABHBGLGALILSF7RELATGIFEVLRKIGRVHTESAGLVIGGKSKE
EEQERLGRMNILVCTPGRMLQHLDQTaLFDTYNLQMLVLDEADRILDLGFQQTVDAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="probable ATP-dependent RNA helicase"
/protein_id="CAD37144.1"
/db_xref="GI:21627812"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(12955. .13492,13553. .13589,13671.
/gene="AfA12H2.05c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(12955. .13492,13553. .13589,13671./gene="AfA12H2.05c"
                                      LESLATGLLG"
                                                                         EEEETLVQLPPYEGDQDDEAPRPSKKPKVKFTEANDREEAEPCDQAAHTPRQIQTLED
                                                                                                           EEQFKARGDAKDQQAKFLAEEAERTRLADMEDKEI AKQKRREKKEKRKARERELLAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             smart:SM00487;DEAD-like helicases superfamily, catalytic
domain;5.6e-53;codon 66-269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain; 8.5e-25; codon 305-388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         smart:SM00490;helicase superfamily c-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16336. .16414)
/gene="AfA12H2.06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(13982. .15673,15761. .15826,15869. .16207,16235. .16311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPESDIKLQYRKKSLLIHPDKTKNPAAPDAFDRLKKAQTTLLDEKARAYLDECIADAR
RLLIREHKYTVDSPELQTEEFKKEWRQKTVQVLLEEEARRRRQLKAKLQEEGREKRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical DNA j domain containing protein"
/protein_id="CAD37143.1"
/db_xref="G1:21627811"
/translation="MSSDEQDALDALEKEASDFIKYCFSIRCVSIILFLYAVLDLQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pfam:PF00226;DnaJ domain;2.9e-10;codon 34-98"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          smart:SM00271;DnaJ molecular chaperone homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="probable FAD synthetase"
/protein_id="CAD37142.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="AfA12H2.06"
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.17294,17367. .17626,17679.
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.17880,17933. .17974,
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Best Local Similarity:
                                                                                                                                                     KEYWORDS
                                                                                                                                                                         VERSION
                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                         LOCUS
                                                                                                                                                                                                                                                                                                                                                                    75008 GGATGCGGCTTGCCAGCTTGGGGGAAGTGT 74979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATTTGCCTTTCTCCTCGAGATGAAACGCAAGTTCCTATCGACCTACCCC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACTCCTATGCACCTCTÇAGCTACATCGTCGTGGCGACCGCCGAACAAGGCCGTCGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AspLeuGlnArgThrIleSerValAspIleArgTyrValLeuPheMet------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCGGTCTGCGGCGGCGGATGTGGTGGAAGAATATCAAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IleGlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluPro 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AsnAsnAspIleThrGlyGlyAsnSerGlySerProValPheAspLysAsnGlyArgLeu 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGACAGAGAATATTGAGCGGGTACTGGAGCGTGGTGAGCGAATTGATTTGTTGGTCGAT 75153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---ThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHisIleAlaPheLeuSer 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PhePheAlaGlyLeuArgGluMet-----
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                                                                                                                                                                                                                                                                                                                                                                                                                 -----IleAspLysTrpGlyGlnCys 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGACTGATCGGCTCGGCGGCAGCGCG------CACGACTTCCGAGTGCGTAGT 75105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---CCGCCGTCGGACTCGCTTCCAGCCCGACGGGAGATCGACAGCGTCCGTGACATT 75213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeuPheArg-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProGlnAspGlyAlaTroTyrAsnTyrHisThrThrGlyLysGlyValLeuGluLysGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGlu
                                                                                                                                                                                                            CNSO1RG9 180688 bp DNA linear PRI 26-JUN-
Human chromosome 14 DNA sequence BAC R-638I2 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
ar.173871
                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Euthéria; Primates; Catarrhini; Hominidae, 1 (bases 1 to 180688)
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AL157871.5
                                                                                                     Homo sapiens
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                                                                                                                           uman
                                                                                                                                                  HTGS_ACTIVEFIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18033. 18181,18245. 18709,18759. 19248)
//gene="AfA1212.07"
//gene
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  Petit, J.L., Vico, V.,
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91.50
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  Dasilva, C., Robert, C., Wincker, P.,
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                                                                         Euteleostomi;
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                                                                                                                    86726. .86933
/note="matching
RHdb:RH68412
87142. .87270
/note="matching
RHdb:RH25853
                                                                                                                                                                                                                                                                                                                 Identified using 85576. .85699
                                                                                             dbsTs:sTS48319
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                                          Identified using the e-PCR software 37142. .87270
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/db_xref="taxon:9606"
                                                                                                                                                                         Identified using 36726. .86933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="R-638I2"
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                         EMBL: T78109
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                                                                                                                                          EMBL: H38818
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Web: www.genoscope.cns.fr)On Jun 27, 2001 this sequence version replacedGenome Center
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Assembly program: Phrap; version 2.0 Quality coverage: 6.78x in Q20 bases; sum-of-contigs
                                                             Downstream BAC (overlapping the SP6 end) : R-362L22 (AC=AL135838)
                                                                                                                        The following BAC sequence is oriented from the T7 to the Upstream BAC (overlapping the T7 end): R-775G15
                                                                                                                                                                                                                      Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (26-JUN-2001) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
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                                                                                                                                                                             PheThrMetArgMet----
                                                                                                                                                                                                                                        LeuPhePheAlaGlyLeuArgGluMetTyrProGlyArgAlaLeuProSerAspAlaAsn 47
                                                        AspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeuPheArgThrLys 101
                                                                                          CCTGTCCAAGGC--
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99113. .99287
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RHdb:RH70848
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1 (bases 1 to 187710)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F., Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Gyapay,G., Saurin,W. and Weissenbach,J.

Sequencing of the human chromosome 14
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                                                                                                                                                                                                                                                                                                                                                                                                        - Web : www.genoscope.cns.fr)
On Oct 5, 2001 this sequence version replaced gi:13872725.
                                                                                                                                                                                                                                                                                 The following BAC sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end) : C-2644I21 (AC-AL163974)

Downstream BAC (overlapping the SP6 end) : R-638I2 ----------
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Human chromosome 14 DNA sequence BAC R-362L22 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
                                                                                                                                                                                                                                       Assembly program: Phrap; version 2.0 Quality coverage: 6.92x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                            Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                          Center: Genoscope / Centre
Center code: GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (04-OCT-2001) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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116864, .117047
/notee="matching EMBL:AA085408
RHdb:RH65341
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171231. .171463
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                                                                                          Avian infectious bronchitis virus s
Avian infectious bronchitis virus
Viruses; ssRNA positive-strand virus
Coronaviridae; Coronavirus.
1 (bases 1 to 1554)
Sapats, S.I., Ashcon, F., Wright, P.J.
Novel variation in the N protein of
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2 (bases 1 to 1554)
Sapats, S.I., Ashton, F.,
Direct Submission
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Direct Submission
Submitted (14-JAN-1997) Sandra I. Sapats,
Submitted (14-JAN-1997) Sandra I. Sapats,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sapats, S.I., Ashton, F., Wright, P.J. and Ignjatovic, J.
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/protein_id="AAB48161.1"
/protein_id="AAB48161.1"
/db_xref="G1:1515373"
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GTGEMGPMDDVWWKAKGADTSKIGNYGVRDPDKFDGAFLFIEGGPNUFRWDFIAL
SRGRNGSSSLATSRESSRFGSRDSSKGGRKKGKAPNFGDDKMIEEGVKDGRLTAMLNLV
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Best Local Similarity:
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Other publication FI 960428 960328
Other publication NO 960332 960321
Other publication CA 2167936 951207
Other publication AU 2675795 951221
Other publication FR 2720408 951201
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                                                                                                                                                                                                                                                                                                 Submitted (03-AUG-1995) Legrain 1
11, rue de Molsheim, Strasbourg,
                                                                                                                                                                                                                                                                                                                                                                                              Neisseria.

1 (bases 1 to 2163)

Legrain, M., Findeli, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis.
Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tbp2;
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                                                                                                                                                                                                                                                                                                                                   Legrain, M.
                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                    ທ
                                                                                                                                                                                                                                                                                                                                             (bases 1 to 2163)
                                                                                                                                                                                                                                                                                                                                                                  from Neisseria meningitidis
Transferrin-binding
                                                                                                                                                                                                                                                                                                                         Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .1 GI:1177568
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                                                                                                                                             /product="transferrin-binding protein
/protein_id="CAA90598.1"
/db_xref="GI:1177569"
                                                                                                                                                                                                                                                       /organism="Neisseria meningitidis"
/strain="BZ163"
                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                 /gene="tbp2"
                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                       'gene="tbp2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
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gene (strain BZ163).
                                                                                                                                                                                                                                                                                                                                                                                                                                  subdivision; Neisseriaceae;
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                                                                                                                                                                                                                                                                                                 M., Transgene, Molecular
Bas-Rhin, France, 67000
                                                                                                                                                                                                                                                                                                                                                                              transferrin-binding protein
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                                   Isogai, T.,
                                                                               Homo sapiens
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US-10-008-355-2_COPY_522_712 (1-191) x NMTBP2163 (1-2163)
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oligo capping; fis (full insert sequence).
Homo sapiens teratocarcinoma cell_line:NT2
clone_lib:NT2RP2 clone:NT2RP2005168.
Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Pujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A.
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3006 apiens cDNA FLJ12944 fis, clone NT2RP2005168, highly sapiens mRNA for EIB-55kDa-associated protein.
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61. .2133
/gene="tbp2"
/product="transferrin-binding
a 480 c 529 g 448 t
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                                                                                                                                                                                                            Sugiyama, T.,
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                                                                                                                                                                                                                                                                                                                          Homo.
                                                         Yamamoto, J.,
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hly similar
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                                                                                                                                                                                                                                                                                                                                                    685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               514 AGCTATGGGGTCAGAAGGGGCCGTGTATGCTTCGAGATGAAGATCAATGAGGAAATCTCC 573
                                                                                                                                                                                                                               111 GlnLeuHisIleAlaPheLeuSerAsnAsnAspIleThrGly---------
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                                                                                                                                                                                                                                                                                                                                                                         ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln 91
                                                                                                                                                                                                                                                                                            GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGly---ArgTyrAlaGluAsnGly 110
                                                                                                                                                                                                                                                                                                                                                                                                                             GACTCCTGCAGCACCCAGCTAGGCGAAGAGCCTTTCTCC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGAAGCACCTTCCGTCTACAGAGCCTGACCCCCACGTGGTCCGTATCGGCTGGTCCCTG 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyArgAlaLeuProSerAspAla-----AsnPheThrMetArgMet------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPro
                                           CGAATCCAGAAGGAAGCCTTGGGGGGGTCAGGCCCTCTATCCTCATGTCCTGGTGAAGAAT 897
                                                                                                                    TGTGGAAATGACGTGGAACTGTCTTTTACCAAGAATGGAAAGTGGATGGGCATTGCTTTC
                                                                                                                                      ---GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPhe 143
                                                                                                                                                                                                                                                                                                                                                  ---SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis 71
                                                                               AspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThr 163
                                                                                                                                                                                             ------AACGATGTGATTGGCTGCTTTGCGGATTTTGAA 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 2794)
1 sogai, T. and Otsuki, T.
1 sogai, T. and Otsuki, T.
Direct Submission
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@fri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEDO human cDNA sequencing Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Tokyo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="cloning vector: pME18SFL3-mRNA from NT2 neuronal
precursor cells after 2-weeks retinoic acid (RA)
induction."
851 c 735 g 521 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="NT2RP2005168"
/cell_line="NT2"
/cell_type="teratocarcinoma"
/clone_lib="NT2RP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
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                                                                                                                                                                                                                                                                        -----AGCCGGTTTGAAAACTACGGAGACAAGTTTGCAGAG------ 744
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89.50
38.32%
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                                                                                                                    837
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898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be for
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 55 Row: i Column: 3
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.nisc.nih.gov/
Contact: nisc_mgcGnhgrl.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Massello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NLSC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC021506 2908 bp mRNA linear ROMUS musculus, Similar to EIB-55kDa-associated protein MGC:33621 IMAGE:5347099, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: h
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 2908)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BC021506.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the following selection criteria: GenomeScan gene
EPDPHVVRIGWSLDSCSTQLGEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFA
DPECGNDVELSTKNGKWMGIAFRIQKEALGGQALY PHVLVKKAVEFNFGGREPYC
SVLPGFTFIQHLPLSERIRGTIGPKSKAECEILMWGLPAAGKTTWAIKHAASNPSKK
YNILGTNAIMUKMRVMGLRRQRNYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQK
NVYGSAQRRKMRPFEGFQRKAIVICPTDEDLKDRTVKRTDEEGKDVPDHAVLEMKANF
                                                                                                                                                                                                      ERELEADDDDGLPGHNNEEVETTEGGSELEGT%QPPPPGLQPHPEPGGYSGPDGHYVMD
NITRONOFYETPVIKOENESSYDRRPLDMEPGQQVYHPEKTEMKQEAPPSFLPPEAS
OLKTDRPQFONKKRPPEENHRGRGYFEHREDRRGRSPQPPAEEDEDDFDDTLVALDTYN
CDLHFKVARDRSSGYPLTIEGFAYLMSGARASYGVRRGRVCFEMKINEEISVKHLPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="MGC:36621 IMAGE:5347099"
/tissue_type="Mammary tumor. C3(1)-Tag model.
ductal carcinoma. 5 month old virgin mouse."
                                                                                                                                                                                                                                                                                                                                                                                                    /product="Similar to ElB-55kDa-associated protein /protein_id="AAH21506.1" /db_xref="GI:18204832"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NCI_CGAP_Mam6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                          translation="MDVRRLKVNELREELQRRGLDTRGLKAELAERLLAALEAEEPED/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .ocation/Qualifiers
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                                                                                                            REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                 TGTGCTGTGGAATTTAACTTT 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTGGAAATGATGTGGAGCTTTCTTTTACCAAGAATGGCAAGTGGATGGGCATTGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPhe 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGAAGCATCTTCCATCT'ACAGAGCCCGACCCCCACGTTGTCCGTATTGGCTGGTCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGAATCCAGAAAGAGGCCTTAGGGGGGTCAGGCCCTCTATCCTCATGTCCTGGTGAAGAAT 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGly---ArgTyrAlaGluAsnGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACTCTTGCAGCACTCAGCTAGGTGAAGAGCCTTTTTTCC-----TATGGTTATGGA 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyArgAlaLeuProSerAspAla-----AsnPheThrMetArgMet-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                   IleSerValAspIleArgTyr 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThr 163
                                                                                                                                                                                                           Homo sapiens, Similar to ELB-55kDa-associated protein MGC:16645 IMAGE:4123077, mRNA, complete cds. BC027713 BC027713 GI:20379473 MGC.
Submitted (08-AFR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 2956)
                                                                 Strausberg,R.
Direct Submission
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                                                     AGCTATGGGGTCAGAAGGGGCCGTGTATGCTTCGAGATGAAGATCAATGAGGAAATCTCC
GlyArgAlaLeuProSerAspAla-----AsnPheThrMetArgMet-----
                                                                                                         AlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPro
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Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Laric,P., Legaspi,R., Maduro,O.L.,
Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J.,
Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C.,
Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Nation Sequencing Center (NISC),
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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NNRGSYNRAPQQQPPPPQQPPPPQQPPPPPSYSPARNPPGASTYNKNSNIPGSSA
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/protein_id="AAH27713.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="MGC:1665 IMAGE:4123077"
/tissue_type="Muscle, rhabdomyosarcoma"
/clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
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/db_xref="taxon:9606"
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                                                                             through
Series:
                                                                                                                                                                   Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Karlins,E., Legaspi,R.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McCDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tlongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                          Gaithersburg, Maryland;
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Submitted (02-JUL-2001) National Institutes of
Gene Collection (MGC), Cancer Genomics Office,
Institute, 31 Center Drive, Room 11A03, Bethesd
                                                                                                                                                            Zhang, L.-H. and Green, E.D.
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1. (bases 1 to 3048)
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BC009988
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                                                      the I.M.A.G.E. Consortium/LLNI
IRAL Plate: 26 Row: h Column:
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
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6 IMAGE:4127873, mRNA,
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                                                                                            information can be found http://image.llnl.gov
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Best Local Similarity:
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                                                                                                                                                                                                              GlnLeuHisIleAlaPheLeuSerAsnAsnAspIleThrGly----
TGCGCAGTGGAGTTCAACTTC
                          IleSerValAspIleArgTyr 170
                                                                                                                                                                                                                                                             GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGly---ArgTyrAlaGluAsnGly 110
                                                                                                                                                                                                                                                                                                                              ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln
                                                                                                                                                                                                                                                                                                                                                                 GACTCCTGCAGCACCCAGCTAGGCGAAGAGCCTTTCTCC----TATGGCTATGGA
                                                         CGAATCCAGAAGGAAGCCTTGGGGGGGTCAGGCCCTCTATCCTCATGTCCTGGTGAAGAAT 111:
                                                                                     AspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThr 163
                                                                                                                                                                                                                                                                                                                                                                                                                            GTGAAGCACCTTCCGTCTACAGAGCCTGACCCCCACGTGGTCCGTATCGGCTGGTCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyArgAlaLeuProSerAspAla----AsnPheThrMetArgMet----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCTATGGGGTCAGAAGGGGCCGTGTATGCTTCGAGATGAAGATCAATGAGGAAATCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scores:
                                                                                                                                     -GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPhe 143
                                                                                                                                                                                                                                                                                                                                                                                            SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="MGC:16706 IMAGE:4127873"
/tissue-type="Brain, neuroblastoma"
/clone_lip="NIH_MGC_19"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="Unknown (protein for MGC:16706)"
/protein_id="AAH09988.1"
/db_xref="GI:14603013"
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
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16: sp_bacteriap:*
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Gapop 10.0 , Gapext 0.5
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sp_phage:*
sp_plant:*
sp_rodent:*
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
 sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	و	8	7	6	u	4	w	2		Result No.
38	39	39	39	39	40	40	40	40	41	42	43	48	48	4.00	48	Score
79.2	81.2	81.2	81.2	81.2	83.3	83.3	83.3	83.3	85.4	87.5	89.6	100.0	100.0	100.0	100.0	Query
253	997	996	499	396	497	363	353	315	284	169	217	716	357	342	316	Match Length DB
ν	w	ω	10	12	16	11	11	16	N	16	N	16	N	16	N	DB
P96151	074325	Q9P7S1	Q9LK70	Q8VA04	Q92J35	Q62314	Q62313	Q9ZDX8	Q47809	Q8YM87	Q9AJX0	Q9PC94	Q04186	Q99V45	Q9FBG1	ID
P96151 vibrio chol	074325 schizosacch	Q9p7s1 schizosacch	Q91k70 arabidopsis	Q8vaO4 apple stem	Q92j35 rickettsia		Q62313 mus musculu	Q9zdx8 rickettsia	Q47809 enterococcu	Q8ym87 anabaena sp	Q9ajxO staphylococ	Q9pc94 xylella fas	Q04186 staphylococ	Q99v45 staphylococ	Q9fbg1 staphylococ	Description

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caeno	O53775 mycobacteri Q9upn5 homo sapien	Q9ns14 homo sapien	Q98xC9 rnizodium i		Q93560 caenorhabdi	Q8y3y8 listeria mo	homo sapien				\rightarrow			Q9kh49 staphylococ	0		ß		Q9srp2 arabidopsis		Q9fyl4 arabidopsis	vib		Q8qr15 apple stem	Q98mq8 rhizobium 1

ALIGNMENTS

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TGGNSGSPV

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1D 00418
AC 00411
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AC 0041
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Best Local
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                                                                                                                                                                                                                                                                                    Q04186 PRELIMINARY; PRT; 357 AA.
Q04186; Q14186; Q1.
Q1.NOV-1996 (TrEMBLrel. 01, Created)
Q1.NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1.MAR-2002 (TrEMBLrel. 20, Last annotation update)
Glutamic acid specific protease prepropeptide (EC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Murakami H., Hosoyama A., Murakami H., Hosoyama A., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; "Whole genome sequencing of meticillin-resistant Staphylococcus aureus.";
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Q99V45;
Q1-JUN-2001
01-JUN-2001
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SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM;
PROSITE; PS00672; V8_HIS; 1.
PROSITE; PS00673; V8_SER; 1.
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                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                            Staphylococcus aureus
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SEQUENCE
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InterPro; IPR000126; Ser_proteas_V8.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00839; V8PROTEASE.
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Cui L., Oguchi A., Aoki K.-I., Nagai Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-S.aureus (strain Mu50), and S.aureus (strain N315); MEDLINE-21311952; PubMed-11418146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                          Yoshikawa
                                                                                                                                                   NCBI_TaxID=1280;
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   Tsuzuki H.,
Shin M., Yo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Serine protease; Complete proteome 36977 MW; 5AEF42DCE01C4B24 CRC64;
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                                                                                                                                                                                                                     Bacillus/Clostridium group; Bacillales,
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Bacillus/Clostridium group; Bacillales;
   H., Fujiwara
Yoshida N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEASES,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48; DB Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
   T., Nakamura
Teraoka H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                   (E)
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                                                                                                                                                                                                                                                                                                       3.4.21.19).
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                                      Iwamoto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT
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Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9PC94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutlino L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Franco S.C., Franco M.C., Fronce M., Furlan L.R.,
                                                                "The genome sequence of the Nature 406:151-159(2000). EMBL; AE004008; AAF84693.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50240; TRYPSIN_DOM; PROSITE; PS00672; V8_HIS; 1. PROSITE; PS00673; V8_SER; 1.
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InterPro; IPR00126; Ser_proteas_V8.
Pfam; PF00089; trypsin; IPR00126; PRINTS; PR00839; V8PROTEASE.
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EMBL; D00730; BAA(
MEROPS; S01.269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simpson A.J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20365717;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xylella fastidiosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Purification, characterization and gene cloning of a novel glutamic acid-specific endopeptidase from staphylococcus aureus atcc 12600."; Biochim. Hophys. Acta 1121:221-228(1991).
Hypothetical protein; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2371;
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9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reinach F.C., Arruda P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed-10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357
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57 POTENTIAL
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-21595285; PubMed-11759840;

Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T

Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

Kishida Y., Kohara M., Sugimoto M., Takazawa M., Yamada M.,
                                                                                                                                                        01-MAR-2002
01-MAR-2002
01-MAR-2002
                                                                                                                                                                                        Q8YM87
Q8YM87;
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                                                                                                    Anabaena sp. (Strut...
Racteria; Cyanobacteria;
                                                                                                                                     ALR5049.
                                                                                                                                            Hypothetical protein
                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
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Bacteria; Firmicutes; Baci
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InterPro; IPR00126; Ser_proteas_V8.
Pfam; PF00089; trypsin; IPR00126;
PRINTS; PR00839; V8PROTEASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Extracellular serine proteinase precursor (Fragment).
                                                                                                   NCBI_TaxID=103690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; S01.269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1282;
                                                                                                                                                                                                                                                           167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis extracellular serine proteinase."; ubmitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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9; Conser
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2 (TrEMBLrel. 20, La:
2 (TrEMBLrel. 20, La:
all protein Alr5049.
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llarity 100.0%;
Conservative (
                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                              (strain PCC 7120).
anobacteria; Nostocales;
                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79375
                                                                                                                                                                                                                                                                                                                                             23667 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus/Clostridium
                                                                                                                                                    20, Created)
20, Last sequence up
20, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                            POTENTIAL.

EXTRACELLULAR SERINE PROTEINASE.

FB9B886D453B8BB7 CRC64;
                                                                                                                                                                                                                                                                                                              Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; I
Pred. No. 2.
                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAF086E2315BBDFC CRC64;
                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                              Nostocaceae; Nostoc
                                                                                                                                                                                                   169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217
                                                                                                                                                                                                                                                                                                             DB 2
6.7;
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                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    group; Bacillales;
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                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                       217;
                                               Ξ,
                                                                                                                                                                                                                                                                                                 0;
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RRR OCC OC DET DAC
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Best Local S
Matches 8
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                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                Q9ZDX8
Q9ZDX8;
Q1-MAY-1999
01-MAY-1999
01-JUN-2002
Protease DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q47809;
01-NOV-1996
01-NOV-1996
01-JUN-2002
                                                                                                                                                                                                                                                                                                                          Submitted (JUN-1992) to the EMBL/Ger
EMBL; 212296; CAA/8168.1; -.
InterPro; IPR001254; Ser_protease_Ti
InterPro; IPR000126; Ser_proteas_V8
PRINTS; PR00839; V8PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q47809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."; DNA Res. 8:205-213(2001).
EMBL; AP003598; BAB76748.1; -.
SEQUENCE FROM
STRAIN-MADRID
                                       Bacteria; Proteobacteria;
Rickettsiaceae; Rickettsi
                                                             Rickettsia
                                                                                                                                                                                                                                                                         PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00672; VB_MIS; 1.
PROSITE; PS00673; VB_SER; UKNOWN_1.
Hydrolase; Serine protease.
SEQUENCE 284 AA; 31063 MW; D4F03:
                                                                                                                                                                                                                                                                                                                                                                                 resembles serine proteinase strain V8.";
                                                                                                                                                                                                                                                                                                                                                                                                   "A gene (sprE) downstream of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecalis (Streptococcus faecalis). Bacteria; Firmicutes; Bacillus/Clostridium grou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcal serine proteinase homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Complete proteome.
SEQUENCE 169 AA; 17427 MW; 0A610CC04EE4C48A CRC64;
                             NCBI_TaxID=782;
                                                                        RP186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPRE.
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-OG1-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcaceae; Enterococcus.
                                                                                                                                                                                       224 TGGQSGSPI 232
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                                                                                                                                                                                                                                Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tabata S.;
                                                             prowazekii.
                                                                                (TrEMBLrel.) (TrEMBLrel.) (HTRA).
                                                                                                                                                                                                                                                                        Serine protease.
284 AA; 31063 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                    PRELIMINARY;
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E Z
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                                        Rickettsieae;
                                                                                                                                                                                                                                          85.4%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.5%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
                                                                                         10,
10,
21,
                                       alpha subdivision;
eae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                        gelE of Enterococcus faecalis OG1-10 determinant of Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                          Last sequence update)
Last annotation updat
                                                                                                               Created)
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Pred. No.
                                                                                                                                                                                                                                           Score 41;
Pred. No.
                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                          D4F0312BEE778415 CRC64;
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                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                    315
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7.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           group; Lactobacillales;
                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                 Rickettsiales;
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                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                    Length 284;
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                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                0;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q62313
Q62313;
                                      DOMAIN
TRANSMEM
                                                                                          Signal;
SIGNAL
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Trans-golgi network integral membrane protein TGN38A precursor (Trans-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -|- SIMILARITY: TO SERINE PROTEASES, T

EMBL; AJ235270; CAA14652.1; -.

InterPro; IPR001478; PDZ.

InterPro; IPR001940; Protease2C.

InterPro; IPR001254; Ser_protease_Try.

Pfam; PF00089; trypsin; 1.

PRINTS; PR00834; PROTEASES2C.
                                                                                                                    MGD;
                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                            STRAIN-ICR; TISSUE-BRAIN;
MEDLINE-95301533; PubMed-7540170;
Kasai K., Takahashi S., Murakami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            golg1 network protein 1) (TGN38 homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50106; PDZ; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitochondria.";
Nature 396:133-140(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Eriksson A.-S., Winkler H.H., Kurland C.G.;
                                                                              CHAIN
                                                                                                                                             EMBL; D50031;
                                                                                                                                                                                                                                                                                                                  "Strain-specific presence of two TGN38 isoforms and absence of TGN41 in mouse.";
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99039499; PubMed=9823893;
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The genome sequence of Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188
                                                                                                                                                                                                                                                                                                       Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TGGNSGSPV 9
                                                                                                                                                      SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. PRIMAR GOLGI NETWORK. CYCLES BETWEEN THE TRANS-GOLGI NETWORK SURFACE RETURNING VIA ENDOSOMES (BY SIMILARITY). TISSUE SPECIFICITY: WIDELY EXPRESSED.
MISCELLANEOUS: ALSO FOUND IN STRAINS BALB/C, C57BL/6
                                                                                                                                                                                                                        mitted (JUN-2001) to the EMBL/GenBank/DDBJ databases FUNCTION: MAY BE INVOLVED IN REGULATING MEMBRANE TR. FROM TRANS-GOLGI NETWORK.
                                                                                                             ", BAA08757.1; -.
", BC009143; AAH09143.1;
"MGI:105080; Ttgn1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGASGSPV 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conserv
                                                                                                        Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease; Complete proteome. 315 AA; 35033 MW; 2D91A0D54FFBE9A1 CRC64;
18
299
320
346
131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                      270:14471-14476(1995).
298
319
353
349
178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.3%;
                                                                                                      Glycoprotein;
                                                                                                                                                                                               TYPE I MEMBRANE PROTEIN. PRIMARILY IN TRANS-BETWEEN THE TRANS-GOLGI NETWORK AND THE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB Pred. No. 33; 0; Mismatches
         CYTOPLASMIC (POTENTIAL).
ENDOCYTOSIS SIGNAL (BY SIMILARITY).
                                                                            TRANS-GOLGI NETWORK INTEGRAL
                                                  EXTRACELLULAR
                                                                PROTEIN TGN38A.
                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prowazekii and the origin
                                                                                                      Repeat;
                                                                                                                                                                                                                                                                                                                                              Nakayama K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRYPSIN FAMILY.
TANDEM
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                                                  (POTENTIAL).
REPEATS
                                                                                                   Golgi stack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                    TRAFFIC TO
                                                                                                                                                          AND DBA/2
                                                                              MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Best Local S
Matches 7
                        Query Match
Best Local
  Matches
                                                                                                      REPEAT
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 270:14471-14476(1995).

-: FUNCTION: MAY BE INVOLVED IN REGULATING MEMBRANE TRAFFIC TO AN PROMITEN STATE OF THE TRANS-COLGI NETWORK.

-: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. PRIMARILY IN TREGULAR LOCATION: TYPE I TRANS-GOLGI NETWORK AND THE GOLGI NETWORK. CYCLES BETWEEN THE TRANS-GOLGI NETWORK AND THE SURFACE RETURNING VIA ENDOSOMES (BY SIMILARITY).

-: TISSUE SPECIFICITY: WIDELY EXPRESSED.

-: NISCELLANEOUS: NOT FOUND IN STRAINS BALB/C, C57BL/6 AND DBA/2.
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Q62314;
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REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                      DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Trans-golgi network integral membrane protein TGN38B precursor (Trans-golgi network protein 2) (TGN38 homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95301533; PubMed-7540170;
Kasai K., Takahashi S., Murakami
"Strain-specific presence of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-ICR; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                       SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD;
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                           Similarity
  Conservative
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Pred. No.
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Pred. No.
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ENDOCYTOSIS SIGNAL (BY:
7 X 8 AA TANDEM REPEATS
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2826FA9E958C5C27 CRC64;
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EXTRACELLULAR (POTENTIAL).
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Sciurognathi; Muridae;
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  Mismatches
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                                38;
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                                                Length 363;
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   Query Match
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Q92J35;
01-DEC-2001
01-DEC-2001
                                                      SUBMITTED (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF438521; AAL32457.1; .

InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR001052; Pltvir_coat.
Pfam; PF00286; virus_p-coat; 1.
Pfam; PF00286; virus_p-coat; 1.
PRINTS; PR00332; POTEXELCAT: UNKNOWN_1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
PROSITE; PS003418; POTEX_CARLAVIRUS_COAT; UNKNOWN_1.
SEQUENCE 396 AA; 45574 MW; E9237780EEBBC333 CRC64;
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01-MAR-2002
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pROSITE; pS50106; pD; 1.
protease; Complete proteome.
SEQUENCE 497 AA; 55517 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00595; PDZ; 1. Pfam; PF00089; trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE008590; AAL027/2.1; -.
InterPro; IPR001478; PDZ.
InterPro; IPR001254; Ser_protease_Try
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Samson D., Roux V.,
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01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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NCBI_TaxID=781;
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Rickettsiaceae; Rickettsieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-MT32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   viruses; ssRNA positive-strand viruses,
NCBI_TaxID=35350;
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                                                                                                                                                                                                                                                                                                                                                                            Komorowska B., Malinowski T.;
"Diversity of the coat protein
isolates.";
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8; Conserv
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Cossart P., Weissenbach
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      81.2%;
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eae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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Last annotation updat
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Pred. No.
   Score 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4EB5872B552EFC6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          sequence of
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53;
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   DB
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on update)
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ch J., Claverie J.-M.,
   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
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Length 396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u><</u>
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RESULT 14
Q9P7S1
ID Q9P7S
AC Q9P7S
DT 01-OC
DT 01-U
DE Hypot
GN SPACZ
OC SChiz
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Q9LK70
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C Q9LK70;
C Q9LK70;
T 01-OCT-2000 (TrEMBLrel. 15, Created)
T 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
T 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
E Similarity to serine protease.
S Arabidopsis thaliana (Mouse-ear cress).
S Arabidopsis thaliana (Mouse-ear cress).
C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
C Spermatophyta; Magnoliophyta; eudicotyledons; core 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural analysis of Arabidopsis the Sequence features of the regions of 4, TAC and BAC clones.";

DNA Res. 7:217-221(2000).

EMBL; AP000373; BAB01154.1; -...

InterPro; IPR001478; PDZ.

InterPro; IPR001254; Ser_protease_Try.

InterPro; IPR001254; Ser_protease_V8.

Defam. DE0005055. DZ.
                                                                                                                                                                      Q9P7S1
Q9P7S1;
01-OCT-2000
01-OCT-2000
01-JUN-2002
                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical signalling-associated PDZ domain containing
SPAC23G3.12C.
                                      Schizosaccharomyces pombe (Fission yeast).

Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

Schizosaccharomycetales; Schizosaccharomycetaceae;

Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00228; PDZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00595; PDZ; 1. Pfam; PF00089; trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50240; TRYPSIN_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00834; PROTEASES2C. PRINTS; PR00839; V8PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaneko T
                  NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakamura Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDLINE=20363099;
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                                                                                                                                                                                                                                                                                                                                                                                                                 2 GGNSGSPV
                                                                                                                                                                                                                                                                                                                                                                        GGNSGGPV 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JUL-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protease;
499 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Serine protease 56188 MW; 016D41
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87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Pred.
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); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       core 39; DB ced. No. 80; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               016D4BA02CA69BE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thaliana chromosome 4,251,695 bp covered
                                                                                                                                                                                                                                                            996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tracheophyta;
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by ninety
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 15
074325
ID 07432
AC 07432
AC 07432
DT 01-NO
DT 01-NO
DT 01-VO
DE SChiz
OC SCHIC
OC S
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Search completed: December 20, 2002, 12:10:22 Job time: 52.3158 secs
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CSTRAIN-972H-;

ROSTRAIN-972H-;

RA Badcock K., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.;

RA Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AL138854; CAB72237.1; -.

InterPro; IPR00114; HPT_SerP_site.

InterPro; IPR001478; PDZ.

R InterPro; IPR001940; Protease2C.

Pfam; PF00595; PDZ; 1.

R Pfam; PF00595; PDZ; 1.

R PRINTS; PR00B34; PROTEASES2C.

R SMART; SM00228; PDZ; 3.

R PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.

SEQUENCE 996 AA; 110407 MW; A008E51746B05AC3 CRC64;
                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D 074325 PRELIMINARY; PRT; 997 AA.

C 074325;

T 01-NOV-1998 (TrEMBLrel. 08, Created)

T 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

T 01-NOV-1998 (TrEMBLrel. 21, Last annotation update)

T 101-NOV-1998 (TrEMBLrel. 21, Last annotation update)

Hypothetical 111.3 kDa protein C1685.05 in chromosome II.

B Hypothetical 111.3 kDa protein C1685.05 in chromosome II.

S PBC1685.05.

S PBC1685.05.

C Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

Schizosaccharomycetales; Schizosaccharomyceteae;

Schizosaccharomycetales; Schizosaccharomyceteae;

Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                          wood v., Rajandream M.A., Barrell B.G., Hilbert H., Duesterhoeft A.; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

-! SIMILARITY: TO YEAST YUL123W.
EMBL; ALO31154; CAA20053.1; -.
InterPro; IPR001478; PD2.
InterPro; IPR00124; Ser_Protease_Try.
Pfam; PF00089; trypsin; 1.
SMART; SM00228; PD2; 3.
PROSITE; PS50240; TRVPSIN_DOM; 1.
Hypothetical protein.
SEQUENCE 997 AA; 111292 MW; D32D7E3CCAE877AO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4896;
                                                                                                                                      227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :||:|||||
212 SGGSSGSPV 220
                                                                                                                               1 TGGNSGSPV 9
:||:||||
227 SGGSSGSPV 23!
                                                                                                                                                                                                                                                                     Local Similarity nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TGGNSGSPV 9
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                 81.2%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.2%; Score 39; DB 3; Length 996; 77.8%; Pred. No. 1.6e+02; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  Score 39; DB 3; Length 997; Pred. No. 1.6e+02; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                     0;
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Database :
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                               Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on:
                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB seq
                                                                                                                                       977
427.5
89.5
                                                                                                                                                                                                 Score
   83
81
81
77.5
77.5
77.5
74.5
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                                                                                                                                                                                                                                                                                                                                  Issued_Patents_NA:*

1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
3: /cgn2_6/ptodata/
4: /cgn2_6/ptodata/
5: /cgn2_6/ptodata/
6: /cgn2_6/ptodata/
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length: 2000000000
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Ygapop 10.0 , x
Fgapop 6.0 , F
Delop 6.0 , F
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-103-840A-2

4 US-09-103-840A-1
                                                                                                                     US-09-221-0178-726
US-09-221-0178-1045
US-09-058-411-1
US-09-134-001C-1520
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US-09-454-721A-3
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Sequence 1045, Ap
Sequence 1, Appli
Sequence 1520, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
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e 4, Apple e 5, Apple e 6, Apple	equence 1, Applequence 7, Applequence 7, Applequence 7, Applequence 8, Applequence 8, Applequence 16, App	equence 9, Appl equence 52, App equence 52, App equence 1, Appl equence 3, Appl equence 3, Appl equence 7, Appl

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RESULT 1
US-09-221-017B-726
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                                                                                                            APPLICATION NUMBER: PP1182: FILING DATE: 31-DEC-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: PP1546 FILING DATE: 30-JAN-1998
                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
                                                                      FILING DATE: 30-JAN-1390
FILING DATE: 30-JAN-1390
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PP2911
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                 FILING DATE: 09-APR-PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                         FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94304-1018
                   APPLICATION NUMBER:
                                                         09-APR-1998
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10-DEC-1998
              PCT/AU98/01023
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Query Match:
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US-09-221-017B-726
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REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                             1636
                                                                                                                           1576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1974 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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             180 lnCysProArgLeuIleGlnGluLeuLysLeuIle 191
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TELEX: 70614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SerLysSerVallleAlaAlaAlaAlaAlaTeGlnAlaAspAlaMetAlaAsnAlaTyr
                                                                                                                                                                                       lyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspL 160
                                                                                                                                                                                                                                                                                                                    AlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrProGlyArg
                                                             TGCAGCGCACAATCAGCGTGGACATCCGCTACGTTCTCTTCATGATTGACAAATGGGGTC
                                                                           euGlnArgThrIleSerValAspIleArgTyrValLeuPheMetIleAspLysTrpGlyG
                                                                                                                          GTCTTGCTTTCGATGGCAACTGGGAAGCTATGAGTGGTGACATCGAGTTCGAACCCGATC
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                                                                                                                                                                                                                                                                    hrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHisIleAlaPheLeuSerAsnA 120
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AGTGCCCCCGTCTCATCCAAGAGCTGAAGTTGATC 1730
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US-09-221-017B-1045
                                               US-10-008-355-2_COPY_522_712 (1-191) x US-09-221-017B-1045 (1-2384)
                                                                                                 Query Match:
                                                                                                                  Best Local Similarity:
                                                                                                                                 Percent Similarity:
                                                                                                                                                                                   Alignment Scores:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       TOPOLAVOL: DNA (Y-
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TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/I
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/221,017B
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                                                                                                                                                                  No.:
                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 650-813-5600
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APPLICATION NUMBER: PP29
FILING DATE: 09-APR-1998
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                                                                                                                                                                                                                                                                                 ORGANISM:
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CLASSIFICATION:
ADDRESSEE: MUKKADO. CTREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
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                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 1, Application Patent No. 6171854
                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA;
APPLICATION NUMBER: BR 9701774.4
FILING DATE: 11-APF:1997
ATTORNEY/AGENT INFORMATION:
NAME: WHITE JR, PAUL E
REGISTRATION NUMBER: 32011
FORMATION NUMBER: 31200/251
                                                                                                                                                                                                                                                     ZIP: 20005-352.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
COMPUTER: FC-TOS/MS-DOS
COMPUTER: FC-TOS/MS-DOS
                                                                                                                                                                                                                                SOFTWARE: Patentin Rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                 REFERENCE/DOCKET NUMBER: 31 
TELECOMMUNICATION INFÓRMATION: TELEPHONE: (202) 861-3000
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STREET: 1100 New
CITY: Washington
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FILING DATE: April 10, 1998
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E: Intellectual Property Group of

E: PILLSBURY MADISON & SUTRO LLP

1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GALLER, Ricardo
VENTION: VACCINES AGAINST INFECTIONS CAUSED BY YF
VENTION: VITUS; YF INFECTIOUS CDNA, METHOD FOR PRODUCING
VENTION: RECOMBINANT YF VIRUS FROM THE YF INFECTIOUS CDNA
VENTION: PLASMIDS TO ASSEMBLE THE YF INFECTIOUS CDNA
                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version
822-0944
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Query Match:
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                                                                                            GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PELICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
                     NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1520
LENGTH: 1083
TYPE: DNA
                                                                                                                                                                                                                                                                                                                         Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                           Sequence 1520, Application US/09134001C
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ORGANISM: Staphylococcus epidermidis
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ORIGINAL SOURCE:
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TYPE: nucleic acid
STRANDEDNESS: single
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US-09-134-001C-1520

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; NAME/KEY: mat_peptide
; OTHER INFORMATION: nuo
US-09-660-587-3
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Best Local Similarity:
Query Match:
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     Query Match:
DB:
                                 Percent Similarity:
Best Local Similarity:
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                                                                    Score:
                                                                                                Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09660587 Patent No. 6392023 GENERAL INFORMATION:
                                                                                                                                                                                           SEQ ID NO 3
LENGTH: 849
TYPE: DNA
ORGANISM: Ehrlichia canis
                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/261,358
PRIOR FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                          APPLICANT: Yu, Xue-Jie
TITLE OF INVENTION: Homologous 28-kilodalton
TITLE OF INVENTION: Genes of Ehrlichia canis
FILE REFERENCE: D6152CIP2
CURRENT APPLICATION NUMBER: US/09/660,587
CURRENT FILING DATE: 2000-09-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuPheArgThr---LysAsnTyr------------GlyArgTyrAlaGluAsn 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGCTAAAAGAGTATGATCTTACAGGTGAAGAATTT-----GAAGGTCTAATCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAAAGGGGCGCATCCCATGAAAAACATCAAGAAACCCTTTGATTTAAAAGGTAAGTCA 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----HisileAlaPheLeuSerAsnAsnAspIleThrGlyGly 125
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 0.521
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                               Matches:
Conservative:
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FILE REFERENCE: D6152CIP
CURRENT APPLICATION NUMBER: US/09/261,358A
CURRENT FILING DATE: 199-03-03
PRIOR APPLICATION NUMBER: 09/201,458
PRIOR FILING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 3
LENGTH: 849
TYPE: DNA
ORGANISM: Ehrlichia canis
В
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                                                                                                                             Query Match:
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Best Local Similarity:
                                                                                                                                                                                   Score:
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US-09-261-358A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Walker, David
APPLICANT: McBride, Jere
APPLICANT: Yu. Xue-Jie
TITLE OF INVENTION: Homo
TITLE OF INVENTION: Gene
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                                                                                                                                                                                                                                                                            NAME/KEY: mat_peptide OTHER INFORMATION: nu
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No.:
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GAGAAAAAAAGACAACTGTAGTATATGGCTTAAAAAGAAAACTGGGCAGGAGATGCAATA
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McBride, Jere W.
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Query Match:
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                                                                                                                                                             US-10-008-355-2_COPY_522_712 (1-191) x US-08-990-823-39 (1-841)
                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIN Ver. 2.0 SEQ ID NO 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: US 96/10375
EARLIER FILING DATE: 1996-06-14
EARLIER APPLICATION NUMBER: 60/000,254
EARLIER FILING DATE: 1995-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis
TITLE OF INVENTION: immunostimulatory Peptides
FILE REFERENCE: 49086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/08/990,823D CURRENT FILING DATE: 1997-12-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 113
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 841
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Modified base
                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                GGCAAGGTTACTGCCGTCGAGCCCACCGACCAGGGCGCACGAGTGACGATGAGCATCGCC
                                                              GlySerIleLysGlyTyrGluProGlnAsp-----
                                                                                                                               MetTyrProGlyArgAlaLeuProSerAspAlaAsnPheThrMetArg---MetSerTyr
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Matches:
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US-09-103-840A-2
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APPLICANT: FRASER, Claire M.

APPLICANT: VENTER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN

TITLE OF INVENTION: TUBERCULOSIS

FILE REFERENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                       US-10-008-355-2_COPY_522_712 (1-191) x US-09-103-840A-2 (1-4403765)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment
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APPLICANT: FLEISCHMAN, Robert D.
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                                                                                                                                                                                                   205549 CTGTATCCG--
                                                    205651 AGCAACTACAAAATCCCCGTCGATGCCTCGGCGAACGTGCATTCGGTGTCA------
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OTHER INFORMATION: "n" bases at various
OTHER INFORMATION: represent a, t, c or
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Best Local Similarity:
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRATITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
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; Sequence 3, Application
; Patent No. 6296854
; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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; Sequence 2, Application US/09441340
; Patent No. 6448476
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APPLICANT: Peter Pushko
APPLICANT: Michael D. Parker
APPLICANT: Jonathan F. Smith
APPLICANT: Burce J. Crise
TITLE OF INVENTION: Live Attenuated Venezuelan
FILE REFERENCE: Army 146
CURRENT APPLICATION NUMBER: US/09/454,721A
CURRENT FILING DATE: 1999-12-07
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CURRENT FILING DATE: 1999-11-16
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TITLE OF INVENTION: Phosphonate Metabolizing
FILE REFERENCE: 38-21(15303)
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EARLIER FILING DATE: 1998-11-17
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                               Sequence 9, Application US/08433522A Patent No. 6013514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1998-12-07 NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Venezuelan Equine Encephalitis Virus
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APPLICANT:
APPLICANT:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
                                                   TITLE OF INVENTION: HAEMOPHILUS NUMBER OF SEQUENCES: 55
                                                                                     APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
                                                                                                                                                                                                                                                                                                          8363 ACTCCGGAG 8371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                8192 AATGGGCGTTTCACGGTG------CCGAAAGGAGTTGGGGGCCAAGGGAGACAGCGGA 8242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8132 TACACCCATGAGAAACCCCCAAGGCTATTACAGCTGGCATCATGGAGCAGTCCAATATGAA 8193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 ProGlyArg-------AlaLeuProSerAspAlaAsnPheThrMetArg
                                                                                                                                                                                                                                                                                                                                        GluProAsp 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProLysSerAsp---GluPheAla---ValGlnGluAsnIle---LeuAspLeuPheArg 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGCATGTGGAAGGCAAGATCGACAACGACGTTCTGGCCGCGCTTAAGACGAAGAAAGCA 8071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPheAspGly-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microsoft Word
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                                                                        OUTER MEMBRANE PROTEIN
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (416) 595-11
TELEFAX: (416) 595-116
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2989 base pair
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No.:
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REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1383 TTAGCGATAACCTTTGTTGTTGATGCTGGACGACGTTTAACTGTTCGCCAACTTCGC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
1761 ACGAAAAATGATTATGGTACGAGTGTCAATTTGGGTTATACCGAACCCTATTTTACTAAA 1820
                                                                                                                                                                                                                                                                             1533 GGAAAAATTCGCTTAGAT-----CGTACAGGTTTCTTCGAAACAGTTGAAAACCGAATT 1586
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LOCATION:
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                                                                                                                                                                                                                                            96
                                                                                                                                                                                                                                                                                                            76 GlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeu 95
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ZIP: M5G 1R7
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STATE: Ontario
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                                                                  GATCCTATCAATGGTAGCAATGATGAAGTGGATGTCGTATATAAAGTCAAAGAACGTAAA 1646
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                                                                                                                                                                                                                                                                                                                                                                                                                     ---TTTGAAGGAAATACCGTTTCTGCTGATAGTACTTTACGTCAGGAAATG-----
                              LeuSerAsnAsnAspIleThrGlyGlyAsnSerGly-----SerProValPheAspLys 134
                                                                                                                                     ACGGGTAGTATCAACTTTGGTATTGGTTACGGT-----ACAGAGAGTGGTATCAGTTAT 1700
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33.88%
21.31%
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                           Best Local Similarity:
Query Match:
                                             US-10-008-355-2_COPY_522_712 (1-191) x US-09-135-166-9 (1-2989)
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                                                                                                                        Percent Similarity:
                                                                                                                                                                      Alignment Scores:
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GENERAL INFORMATION:
APPLICANT: CHONG,
                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (416) 595-110
INFORMATION FOR SEQ ID NO:
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No
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                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2989 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: (
FILING DATE: 12-SEP-1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
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                                                                                                                                                                                                                   NAME/KEY:
16 MetAlaAsnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGlu 35 :::||| ::: ::::: ||||:::|||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
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LOOSMORE, Sheena
SIA, Dwo Yuan Charles
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595-1163
NO: 9:
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Matches:
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US-08-942-046-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
       CLASSIFICATION: 435
PRIOR APPLICATION UMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCE.
CORRESPONDENCE ADDRESS:
CORRESPONDENCE Sim & McBurney
CORRESPONDENCE ADDRESS:
APPROX. 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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ZIP: M5G 1R7
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STEWART, Michael I
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YANG, Yan Ping
LOOSMORE, Sheena
SIA, Dwo Yuan Charles
KLEIN, Michel
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; NAME/KEY:
; LOCATION:
US-08-942-046-9
               US-09-206-942-52; Sequence 52, Application; Patent No. 6432669; GENERAL INFORMATION:
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Best Local Similarity:
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REFERENCE/DOCKET NUMER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR,SEQ ID NO: 9:
SEQUENCE CHARACTERISTIGS:
LENGTH: 2989 base pairs
TYPE: nucleic acid
STEANMENLESS: 6161
APPLICANT: Loosmore, Sheena
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TOPOLOGY: lir
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Matches:
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Search completed: December 21, Job time: 2265 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
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SEQ ID NO 52
LENGTH: 2934
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
TITLE OF INVENTION: Molecular Weight Proteins
FILE REFERENCE: 1038-861 MIS:jb
CURRENT APPLICATION NUMBER: US/09/206,942
CURRENT APPLICATION NUMBER: 09/167,568
EARLIER APPLICATION NUMBER: 09/167,568
EARLIER APPLICATION NUMBER: 09/167,568
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 95
NUMBER OF SEQ ID NOS: 95
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GGCTCTAATCTTACCTTAAATTCCCCATGTTCGCAAGTATAATGCTTTTGAAATCAATAAA
                                          AspLeuGlnArgThrIleSerValAspIleArg---TyrValLeuPheMetIleAspLys 177
                                                                                                                                                                AATATTTCGGTCACTGGCGGA-----GGTTCTGTGTTTTTCGATATATACGCTAACCTT
                                                                                                                                                                                                                                                AGGTTAAAACCAAATGAGAAGACAACTCCTAACAGACCACTACCAATTCAGTTTTTATCT
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                                                                                                                                                                                                                                                                                                                            -----AATGAAATGAAATTTAATATTGGTAATAATGCCAAGGCTGAATTT
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Conservative:
Mismatches:
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Command line parameters:

-MODEL=frame+_p2n.model -DEY=xlh
-Op-Cgn2_1/USPT0_spool/US10008355/runat_17122002_112705_16942/app_query.fasta_1.327
-Op-Cgn2_1/USPT0_spool/US10008355/runat_17122002_112705_16942/app_query.fasta_1.327
-DB=EST -OPMT=fastap -SUPETX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UTEMT=ptc -NORM=ext -HEAP$IZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10008355_eCGN_1_1.763_erunat_17122002_112705_15942 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEY_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1; -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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length: 2000000000
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Ygapop 10.0 , Ygapext
Egapop 6.0 , Egapext
Delop 6.0 , Delext
US-10-008-355-2_COPY_522_712
1003
1 SKSVIAAARNIQADAMANAY.....
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gb_est2:*
gb_htc:*
gb_est3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

į	_	C 44	43	42	41		c 39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	100	οα	, ~	ı o	U	4-	ω	2		Result No.
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ALIGNMENTS

REFERENCE AUTHORS	CNOCHEDR	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	вн400391/с	RESULT 1
Anopheles. 1 (bases 1 to 426) Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J.	Anopheses yamazae Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;	African malaria mosquito.	GSS.	BH400391.1 GI:17346607	BH400391	DNA sequence.	AG-ND-147H4.TF ND-TAM Anopheles gambiae genomic clone AG-ND-147H4,	BH400391 426 bp DNA linear GSS 11-DEC-2001		

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
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                                                                           ArgLeuIleGlyLeuAlaPheAspGlyAsnTrpGluAla 149
                                                                                                                                       LeuSerAsnAsnAspIleThrGlyGlyAsnSerGlySerProValPheAspLysAsnGly 136
                                                                                                                                                                                 TATAAAAAGAAAATTATGGTATGTACAAAGACAAAGACGGGCAACTTCATGTAAACTTC
                                                                                                                                                                                                                                            ATTAAGAAGTACAAGAAAGGTGACGAAGAATTCGATCTTCCACAAGGACTTCTTGATCTT
                                                                                                                                                                                                                                                                        LeuGluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIleLeuAspLeu
                                                                                                                                                                                                                                                                                                                                 LysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyVal 77
                                                                                                                                                                                                                                                                                                                                                                  TATCCGGATGCTAACTCTACGATCAGGTTAACTTATGGTCAGATCGAGACGCTTCCTAAA
                                                                                                                       CTTTCTAATAACGATATTACAGGAGGTAACTCAGGTTCTCCAATTATCGATGGTTACGGA
                                                                                                                                                                                                              PheArgThrLysAsnTyrGlyArgTyrAlaGlu---AsnGlyGlnLeuHisIleAlaPhe 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         partial digest.
Seq primer: M13 For
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 301 838 3543
Email: bjloftus@t
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Other_GSSs: AG-ND-147H4.TR
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 BH371846
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/clone="AG-ND-147H4"
/clone=11b="ND-TAH4"
/clone=1'Vector: pECBAC1; Site_1:
/note="Vector: 76 g 160 t
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US-10-008-355-2_COPY_522_712 (1-191) x
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                                                                                                                                                                                                                                                                                                                                                                  149 AlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThrIleSerValAspIle 168
                                                                                                                                                                                                               LysLeuIle 191
                                                                                                                                                                                                                                                                                                                                           ACTITAGIA 130
                                                                                                                                                                                                                                                           AGATACGTACTTTGGGTAATCGACAAGTTTGCAGGTGCTAAAAACTTAATTAGCGAATTG
                                                                                                                                                                                                                                                                                                 ArgTyrValLeuPheMetIleAspLysTrpGlyGlnCysProArgLeuIleGlnGluLeu 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity:
                    AGENCOURT_6597467 NIH_MGC_41 5', mRNA sequence.
BM562210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shetty, J., Malek, J., Koo, H., Direct Submission of BAC-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anopheles gambiae
Eukaryota; Metazo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AG-ND-162M17.TF ND-TAM Anopheles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             African malaria mosquito
BM562210.1 GI:18808104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 822)
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/db_xref="taxon:7165"
/clone="AG-ND-162M17"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: Hi
a 142 c 155 g 290 t
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                                                             111 GlnLeuHisIleAlaPheLeuSerAsnAsnAspIleThrGly-------
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                                                                                                                                                                                                                                                                                                                                                                                            266 GACTCCTGCAGCACCCAGCTAGGCGAAGAGCCTTTCTCC------
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                                                                                                                                                                    GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGly---ArgTyrAlaGluAsnGly 110
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Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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National Institutes of Health, Mammalian Gene Collection (MGC)
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1. (bases 1 to 1102)
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http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution informat.
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/lab_host="bH10B (phage-resistant)"
/note="forgan: skin: Vector: poTBP; Site_1: XhoI; Site_2:
XhoI; Si
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/clone="IMAGE:5480814"
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                                                                             19 AlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPro
39 GlyArgAlaLeuProSerAspAla----AsnPheThrMetArgMet--
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                                       AGCTATGGGGTCAGAAGGGGCCGTGTATGCTTCGAGATGAAGATCAATGAGGAAATCTCC
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1 (bases 1 to 630)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) upublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP
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602535962F1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:4684958
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                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="amelanotic melanoma, cell line"
/lab_host="PHIOB (phage-resistant)"
/note="Organ: skin; Vector: pOTBF; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT prining. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                          NIH_MGC Library."
155 c 177 g
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/db_xref="taxon:9606"
/clone="IMAGE:4684958"
/clone_lib="NIH_MGC_41"
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	FEATURES Source	AUTHORS TITLE JOURNAL COMMENT	ORGANISM	ACCESSION VERSION KEYWORDS	RESULT 5 BI391728 LOCUS DEFINITION	Qy 164 Db 531	Qy 144 Db 471	Oy 125 Db 411	Qy 111 Db 378	Qy 92 Db 342	Qy 72 Db 318	Qy 53 Db 267	Db 207
/strain="Commercial broiler chicken" /db_xref="taxon:9031" /clone="pgpln.pk005.f8" /clone="pgpln.pk005.f8" /clone="pgpln.pk005.f8" /clone=lib="Normalized Chicken Pituitary/Hypothalamus/Pineal Library" /sex="Male and Female" /tissue=type="Pituitary Gland/Hypothalamus/Pineal Gland" /dev_stage="Embryonic (d12,d14,d19); post-hatch (w1,w3,w5,w7,w9)" /lab_host="E. Coli EMDH10B" /note="wector: pcMvSPoRT6; Library made from equivalent pools of total RNA isolated from each tissue at different ages. Single pass sequencing from 5'-end"	Tel: 302-1 Fax: 302-1 Email: co	Porter, T.E. and Codpurn, L.A. ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA Library USDA/IFAFS Animal Genome Project Unpublished (2001) Contact: Larry A. Cogburn University of Delaware University of Delaware Townsend Hall, Newark, DE 19717, USA		gblaAH04057.11AAH04057 (BC004057) Similar to transforming, acidic coiled-coil containing protein 2 [Mus musculus], mRNA sequence. B1391728.1 GI:15085010 EST.		IleSerValAspIleArgTyr 170 ::: ::: TGCGCAGTGGAGTTCAACTTC 551	AspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThr 163	GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPhe 143 	GlnLeuHisIleAlaPheLeuSerAsnAspIleThrGly	GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGly 110	ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln 91 GCCACTGGGAAG	SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis 71 	:::
foun foun Plat High High FEATURES Source	Emai Tiss cDN cDN DNA	Euka Mamm REFERENCE 1 (AUTHORS NIH- TITLE Nati JOURNAL Unpu COMMENT Cont	ACCESSION BE26 VERSION BE26 KEYWORDS EST. SOURCE huma ORGANISM HOMO	SULT 6 268652 CUS	Db 410 GATCTG Qy 106 TyrAla III	Db 350 AAGTCT Qy 86 AspGlu	Db 296 TATGAG Qy 66 AlaTrp	Db 236 AAAGAG Qy 46 AlaAsn	Db 176 GCTGCA Qy 26 LysArg	US-10-008-355-2_ Qy 6 AlaAla	Percent Similari Best Local Simil Query Match: DB:	Alignment Scores Pred. No.: Score:	BASE COUNT ORIGIN

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 701)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM132 row: C column: 07
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/clone="InAxon:9606"
/clone="InAKBE:3344958"
/clone=Lib="NIH_MGC_8"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
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SOURCE
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                                Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
                                                                                                                                                                            BM838106.1 GI:19194515
EST.
                                                                                                                                                                                                                   mRNA sequence.
BM838106
                                                                                                  Eukaryota;
Mammalia; |
                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                    K-EST0114293 S9SNU601 Homo sapiens cDNA clone S9SNU601-73-C05 5',
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Frontier Korean EST Project 2001
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                                                                                              a; Metazoa;
; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 AlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPro
                                                                                                                                                                              GGCACTGGGAAG------
                                                                                                                                                                                                                                                                                               ---SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis
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                                                                                                                                 GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGly---ArgTyrAlaGluAsnGly 110
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Plate: 73 row: C column: 05
High quality sequence stop: 710.
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Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="organ: Stomach; Vector: pME18-FL3; Site_1: xhoI; Site_2: xhoI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pME185-FL3 vector. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method The cDNA libraries constructed by this method are full-length enriched cDNA library."
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/cell_line="SNU-601"
/lab_host="Top10F'"
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/clone_lib="S9SNU601"
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/db_xref="taxon:9606"
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-AACGATGTGATTGGCTGCTTTGCGGATTTTGAA 378
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Best Local Similarity:
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                                     39
GTGAAGCACCTTCCGTCTACAGAGCCTGACCCCCACGTGGTCCGTATCGGCTGGTCCCTG
                                 GlyArgAlaLeuProSerAspAla-----AsnPheThrMetArgMet------
                                                                       AGCTATGGGGTCAGAAGGGGCCCGTGTATGCTTCGAGATGAAGATCAATGAGGAAATCTCC 162
                                                                                                           AlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IleSerValAspIleArgTyr 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGENCOURT_7566326 NIH_MGC_92 Homo sapiens cDNA clone 5', mRNA sequence.
BQ215538
BQ215538.1 GI:20396938
EST.
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plate: LLAM13284 row: c column: 14
High quality sequence stop: 673.
Location/Qualifiers
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Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                 198
                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/clone="IMAGE:6043333"
/clone_lib="NIH_MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="PH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
98 a 228 c 239 g 186 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnLeuHisIleAlaPheLeuSerAsnAspIleThrGly-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----AACGATGTGATTGGCTGCTTTGCGGATTTTGAA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGly---ArgTyrAlaGluAsnGly 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis
                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl. Plate: LLCM798 row: n column: 03
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                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence start: 24 High quality sequence stop: 790.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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National Institutes of Health, M
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601589315F1 NIH_MGC_7 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
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        202
/lab_host="DH108 (phage-resistant)"
//lab_host="DH108 (phage-resistant)"
//note="Organ: lung: Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 203 c 255 g 193 t
                                                                                                                                                                                                            /clone="IMAGE:394390"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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Primates;
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Catarrhini;
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CDNA
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i; Hominidae; Homo.
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GTGAAGCACCTTCCGTCTACAGAGCCTGACCCCCACGTGGTCCGTATCGGCTGGTCCCTG
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                                                                                                                                                                                                                      881
AGENCOURT_6409930 NIH_MGC_85
5', mRNA sequence.
BM456284
BM456284
BM456284.1 GI:18505324
EST.
                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 881)
                                                                                                                                                                                             Homo sapiens
                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammalian
                                                                                                   Contact: Robert Strausberg, Ph.D
                                                                                                                  Unpublished (1999)
 http://image.llnl.gov
             found through the I.M.A.G.E. Consortium/LLNL
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US-10-008-355-2_COPY_522_712 (1-191) x BM456284 (1-881)
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Best Local Similarity:
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                            AGENCOURT_6392962 NIH_MGC_72
5', mRNA sequence.
BM449938
BM449938.1
EST.
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Location/Qualifiers
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/tissue_type="lymphoma, cell line"
/lab_host-"DH10B (phage-resistant)"
/nab_host-"DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 224 c 256 g 192 t 2 others
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/db_xref="taxon:9606"
/clone="IMAGE:5496635"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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Plate: LLAM12205 row: o column: 15
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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CDNA Library Arrayed by: The I.A.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information ca
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/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Si
Site_2: Sall: Cloned unidirectionally. Pri
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194 t 2 others
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/clone="IMAGE:5528678"
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US-10-008-355-2_COPY_522_712 (1-191) x BQ645307 (1-904)
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                                                                           GTGAAGCACCTTCCGTCTACAGAGCCTGACCCCCACGTGGTCCGTATCGGCTGGTCCCTG 358
                                                                                                                       GlyArgAlaLeuProSerAspAla-
                                                                                                                                                                           AGCTATGGGGTCAGAAGGGGCCGTGTATGCTTCGAGATGAAGATCAATGAGGAAATCTCC 298
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National Institutes of Health, Mammalian
Unpublished (1999)
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Tissue Procurement: CGAP (Stanford)
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-SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis 71
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTBF; Site_1: xhoI; Site_2: EcoRI; cDNA made by oligo-dT priming Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size I.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callfornia, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II.RT (Life Technologies). Note: this is a NIH_MGC
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227 c
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ORIGIN	BASE COUNT	FEATURES Source		REFERENCE AUTHORS TITLE JOURNAL	×	ACCESSION I VERSION I KEYWORDS I	RESULT 13 BQ652808 LOCUS DEFINITION	Qy 164 Ile Db 623 TG	Qy 144 Ası Db 563 CG	Qy 125 Db 503 TG:	Qy 111 Gl ₁ Db 470	Db 434	Db 410 GG Qy 92 G1	72	Db 359 GAG
- -	/organism="Romo Sapiens" /db_xrief="ftaxon:9606" /clone="ib="NHH_MGC:100" /clone="ib="NHH_MGC:100" /tissue_type="hepatocellular carcinoma, cell line" /lab_host="NHH_MGC:100" /lab_host="NHHOBC (phage resistant)" /note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr prinding Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CONA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." 222 a 240 c 275 g 205 t	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llhl.gov Plate: LLCM2509 row: k column: 04 High quality sequence stop:.621. Location/Qualifiers 1942	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: CGAP (Stanford) cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	to 942) p://mgc.nci.nih.gov/. pstlthtes of Health, Mammalian Gene Collect (1999)	human. Homo sapiens Eukaryota; Metaçoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	BQ652808 BQ652808.1 GI:21776980 EST.	BO652808 942 bp mRNA linear EST 15-JUL-2002 AGENCOURT_8490114 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6298491 5', mRNA sequence	IleSerValAspIleArgTyr 170 ::: ::: TGCGCAGTGGAGTTCAACTTC 643	AspGlyAshTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThr 163 	GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPhe 143 	GlnLeuHisIleAlaPh¢LeuSerAsnAsnAspIleThrGly 124 :: AACGATGTGATTGGCTGCTTTGCGGATTTTGAA 502		GGCACTGGGAAG	erAspG	GACTCCTGCAGCAGCCAGCTAGGCGAAGAGCCTTTCTCCTATGGCTATGGA 409
plate: LLAM90234 row: b High quality sequence stop	ORGANISM Mus musculus Eukaryota; Metazoa; Chorda Mammalia; Eutheria; Rodent REFERENCE 1 (bases 1 to 943) AUTHORS NIH-MGC http://mgc.nci.nih TITLE Unpublished (1999) COMMENT Contact: Robert Strausberg Email: cgapbs-r@mail.nih.g Tissue Procurement: Gilber CDNA Library Preparation: CDNA Library Arrayed by: DNA Sequencing by: Incyte Clone distribution: MGC c found through the I.M.A.G. http://image.llnl.gov	LOCUS DEFINITION 602334417F1 NCI_CGAP_Mam1 MRNA sequence. ACCESSION BG174574 VERSION BG174574.1 GI:12681277 KEYWORDS EST. SOURCE house mouse.	Qy 164 IleServalAspIleArgTyr 170 ::: ::: Db 623 TGCGCAGTGGAGTTCAACTTC 643 RESULT 14	Qy 144 AspGlyAsnTrpGluAlaMetSerGlyA	Qy 125GlyAsnSerGlySerProValPhez	Db 470		Qy 72 ThrThrGlyLysGlyValLeuGluLysGl	Oy 53SerTyrGlySerIleLysGlyTyrGlyTyrGlySerIleLysGlySerIleLysGlyTyrGlySerIleLysGlyTyrGlySerIleLysGlyTyrGlySerIleLysGlyTyrGlySerIleLysGlyTyrGlySerIleLysGlyTyrGlySerIleLysGlyTyrGlySerIleLysGlyTyrGlySerIleLysGlyTyrGlySerIleLysGlyTyrGlySerIleLysGlyTyrGlySerIleLysGlyTyrGlyTyrGlySerIleLysGlyTyrGlySerIleLysGlyTyrGlySerIleLysGlyTyrGlySerIleLysGlyTyrGlySerIle	Qy 39 GlyArgAlaLeuProSerAspAla Db 299 GTGAAGCACCTTCCGTCTACAGAGCCTC	Qy 19 AlaTyralaIleGluLysGlyLysArgI ::: ::: ::: ::: Db 239 AGCTATGGGGTCAGAAGGGGCCCTGTAT	US-10-008-355-2_COPY_522_712 (1-191) x	Percent Similarity: 35.32% Best Local Similarity: 25.15% Query Match: 8.92% DB: 14		Alignment Scores:

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n. gov
nert Smith, Ph.D.
n: Life Technologies, Inc.
r: The I.M.A.G.E. Consortium (LLNL)
rte Genomics, Inc.
clone distribution information can be
G.E. Consortium/LLNL at:
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ealth, Mammalian Gene Collection (MGC)
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ntia; Sciurognathi; Muridae; Murinae; Mus.
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                             AspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThr 163
                                                                                                                                                                                                                                                                                                                                                                                GlnLeuHisIleAlaPheLeuSerAsnAsnAspIleThrGly-------
                                                                                                                                                                                                                                                                                                                                                                                                                              GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGly---ArgTyrAlaGluAsnGly 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyArgAlaLeuProSerAspAla----- 52
                          5', mRNA sequence.
BQ646879
BQ646879.1 GI:21771051
EST.
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                                                                                                                                                                                                                                                                                                                     ---GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPhe 143
                                                                                                                                                                                                                                                                                                                                                                                                              ---SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGAAGCATCTTCCATCTACAGAGCCCGACCCCCACGTTGTCCGTATTGGCCTGGTCCTTG
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                                                                                                                                                                                                                             CGAATCCAGAAAGAGGCCTTAGGGGGGTCAGGCCCTCTATCCTCATGTCCTGGTGAAGAAT 512
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AGENCOURT_8342919 NIH_MGC_100
5', mRNA sequence.
              human
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sapiens
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226 c 280 g 209 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4457381"
/clone_lib="NCI_CGAP_Mam1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
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38.32%
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Matches:
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                                                                                          Homo
                                                                                      mRNA linear EST 15-JUL-2002 sapiens cDNA clone IMAGE:6268916
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TITLE
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US-10-008-355-2_COPY_522_712 (1-191) x BQ646879 (1-960)
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                                                                                                                                                                                                                                                                                                                                                                                        72 ThrThrGlyLysGlyValLeuGluLysGlnAspProLysSerAspGluPheAlaValGln 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 AlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrPro 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyArgAlaLeuProSerAspAla-----AsnPheThrMetArgMet------
                                                                                                                                                           GlnLeuHisIleAlaPheLeuSerAsnAsnAspIleThrGly------
                                                                                                                                                                                                                                                      GluAsnIleLeuAspLeuPheArgThrLysAsnTyrGly---ArgTyrAlaGluAsnGly 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACTCCTGCAGCCAGCTAGGCGAAGAGCCTTTCTCC-----TATGGCTATGGA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---SerTyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHis 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGAAGCACCTTCCGTCTACAGAGCCTGACCCCCACGTGGTCCGTATCGGCTGGTCCCTG 358
                                                                                                 -----AACGATGTGATTGGCTGCTTTGCGGATTTTGAA 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 960)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: LLCM2441 row: j column: 21 High quality sequence stop: 660.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: CGAP (Stanford)
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-GlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIleGlyLeuAlaPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NH_MCC_100"
/clone_lib="NH_MCC_100"
/tissue_type="hepatocellular carcinoma, cell line"
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/lab_host="PHH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NHH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6268916"
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Result
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-Q-/cgn2_1/USPTO_spool/US310008355/runat_17122002_112705_17000/app_query.fasta_1.327
-DB-Published_Applications_NA -QFMT-fastap -SUFFIX=p2n.rnpb -MINMATCH-0.1
-LOOPCL-0 -LOOPEXT-0 -UNITS-bits -START=1 -END=-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER-US10008355_@CGN_1_1_21 @runat_17122002_112705_17000
-NCPU-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
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     1003
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81.5
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length: 2000000000
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356696 seqs, 198428768 residues
                                                                                                                                                                                                                                              : /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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:/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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0 US-09-770-149-525
0 US-09-815-242-4296
0 US-09-815-242-8179
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1284.742 Million cell updates/sec
Sequence 1, Appli
Sequence 525, App
Sequence 4296, Ap
Sequence 8179, Ap
                                                                                       Description
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US-10-008-355-1
                                                       Score:
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ALIGNMENTS

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SSQUENCE 1, Application US/10008355

Patent No. US20020164759A1

GENERAL INFORMATION:
APPLICANT: Patents, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
PILE REFERENCE: 235.00440101

CURRENT APPLICATION NUMBER: US/10/008,355

CURRENT FILING DATE: 2000-11-08

PRIOR APPLICATION NUMBER: US 60/246,827

PRIOR FILING DATE: 2000-11-08

PRIOR FILING DATE: 2000-11-08

PRIOR APPLICATION VERSION 3.0

SEQ ID NO 1

LENGTH: 2139

TYPE: DNA

ORGANIZSM: POTPHYTOMONAS GINGIVALLS

LONGANIZSM: POTPHYTOMONAS GINGIVALLS

CORGANIZSM: POTPHYTOMONAS GINGIVALLS

Pred. No.:

1.03e-123

Pred. No.:
1.03e-123

Matches:
191

Percent Similarity: 100.00%

Mismatches: 0

Query Match: 00

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                                                                                                                                                                                                                                                                                            Sequence 525, Application Patent No. US20020059663A1 GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences (
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
                                                                         APPLICANT:
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                                                                                                                                             Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
                                                                                                       Garcia, Carlos A.
Kricker, Maja
Slader, Ted
                                                                                   Davis, Keith R. Allen, Keith
                                                                                                                                                                                                          Yu, Yang
Rameaka, Joshua G.
                                                                                                                                                                                                                                 Raines, Tracy
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Best Local Similarity:
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                                             APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T
APPLICANT: Xu, H. Howard
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SEQ ID NO 525
LENGTH: 651
TYPE: DNA
                                                                                                                                             Sequence 4296, Application Patent No. US20020061569A1 GENERAL INFORMATION:
TITLE OF INVENTION: Identification of ESSITITE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA. 011A
CURRENT APPLICATION NUMBER: US/09/815,242
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PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
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                                                           Carr, Grant J.
Yamamoto, Robert T.
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85.50
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US-10-008-355-2_COPY_522_712 (1-191) x US-09-770-149-525 (1-651)
474 ATTGACACAGTTGTCCGAACAGTTCCGTACCTCATT
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                                                                                                                                                        GGGCCATTGCTTGATTCTTATGGCCATACCATAGGTGTGAACACTGCCACATTCACCCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspAlaAsnPheThrMetArgMetSerTyrGlySerTleLysGlyTyrGluPro---Gln
                                                                              AAAGGGAGTGGTATGTCTTCTGGTGTTAACTTT-----
                                                                                                     AsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThrIleSer
                                                                                                                                                                                             SerProValPheAspLysAsnGlyArgLeuIleGlyLeu-----
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Matches:
Conservative:
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8 27 65
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2001-03-21

60/206,848 60/191,078

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RESULT 4
US-09-815-242-8179
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
Sequence 8179, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
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LENGTH: 720
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PRIOR APPLICATION NUMBER: 60/-
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/-
PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                         691
                                                                                                                                                                                        161
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DR FILING DATE: 2000-05-26
DR FILING DATE: 2000-10-23
DR FILING DATE: 2000-10-23
DR APPLICATION NUMBER: 60/253,625
DR FILING DATE: 2000-11-27
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aAAAAGTTCATTGCAGAAAACATA 714
                                                                                                                                                                                                                                                                                                       ACTGAAAGT----
                                                                                                                                                                                                                                                                                                                                                                                                                        CATGAGTCAACTGGTCCTGTGATGTCAGTAGAAGGTAGCAGCATTGTATATTCAGCGCAT 561
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                                                                                                                                                                                                                                                       -----AspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeu 160
                                                                                                                                                                                                                                                                                         TCTGGATCACCTGTATTAAACAGCAACAACGAATTAATAGGTATTCATTTTGCTTCTGAT
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81.50
37.34%
22.97%
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Matches:
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Query Match:
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PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 8179
LENGTH: 765
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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LOCATION: (1)
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ORGANISM: Staphylococcus
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364 TATCCAGGTAAAGAAGATGTATCAGTTCAAGTTGAAGAGGGGTGCAATAGAACGTGGT
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 GTAAAAATGATGACAACAGAAATGCATATGGC-----
                               -----AspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGluProAspLeu 160
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Xu, H. Howard
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161 GlnArgThrIleSerValAspIle 168

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APPLICANT: NAME, AND METHODS OF PLA TITLE OF INVENTION: STRESS-REGULATED GENES OF PLA TITLE OF INVENTION: STRESS-REGULATED GENES OF PLA TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-05-26

INUMBER OF SEQ ID NOS: 5379

SEQ ID NO 2020

LENGTH: 1812

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US-09-938-842A-2020
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DB:
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                                                                                                                                                                                     -----AspIleThrGlyGlyAsnSerGlySerProValPheAsp------LysAsn 135
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Best Local Similarity:
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SEQ ID NO 3
LENGTH: 849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Walker, David H.
APPLICANT: WcBride, Jere W.
APPLICANT: Yu, Xue-Jie
TITLE OF INVENTION: Homologous 28-Kilodalton Immunodominant protein
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
FILE REFERENCE: D6152CIP2/D1
CURRENT APPLICATION NUMBER: US/10/062,624
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 09/660,587
PRIOR APPLICATION NUMBER: 09/660,587
PRIOR FILING DATE: 2000-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: mat_peptide
OTHER INFORMATION: nuc
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                                                                                                                                                                                                                                                         57 IleLys-----GlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThrThrGly 74
                                                                                                                                                                                                                                                                                                                                       43 ProSer------AspAlaAsnPheThrMetArg------MetSerTyrGlySer 56
                                                                                                                                                                                                                                                                                                                                                                                                                    23 GluLysGlyLysArgLeuPhePheAlaGlyLeuArgGluMetTyrProGlyArgAlaLeu 42
                                                                                LeuAspLeuPheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHisIle 114
                  AlaPheLeuSerAsnAsnAspIleThrGlyGlyAsnSerGlySerPro----
                                                         TATGAAGCATTTGATGTGAAAAATCCAGGTGATAATTACAAAAACGGTGCTTACAGGTAT 423
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Query Match:
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APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/974,300 CURRENT FILING DATE: 2001-10-05 PRIOR APPLICATION NUMBER: 09/680,598
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No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProSerAspAlaAsnPheThrMetArgMetSerTyrGlySerIleLysGlyTyrGluPro
SerGlyAspIleGluPheGluProAspLeuGlnArg 162
                                  CCGACGGCG---GACGGCAAAACCGTTCCGTTCGTGCCGGGAAAAACGTGG-----
                                                                                                                                                                                                                                                                                                                                                                                                           ACAAACCGTGTCGAATATGGTTATGATAAAAAGGTTGAAGGCTATGTGAGAAAGTCAGAC
                                                                       GlyLeuAlaPheAspGly----
                                                                                                                                            AsnAspIleThrGlyGlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIle 139
                                                                                                                                                                                   TCAGGCGGAAAAGGACTCCTTCTGCAAAACGGGGAAGTCCATCGGATCAGCTGGAAGAAC
                                                                                                                                                                                                                     ThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHisIleAlaPheLeuSerAsn 119
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; NAME/KEY: misc_feature
; LOCATION: (1)..(841)
; OTHER INFORMATION: n is a,
US-09-996-634-39
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US-09-996-634-39
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PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR APPLICATION NUMBER: US 96/10375
PRIOR FILING DATE: 1996-06-14
PRIOR FILING DATE: 1995-06-15
PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
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TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
FILE REFERENCE: 61260
CURRENT APPLICATION NUMBER: US/09/996,634
CURRENT FILING DATE: 2001-11-28
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147 TrpGluAlaMetSerGlyAspIleGluPheGluProAspLeuGlnArgThrIle 164
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                                    TCCAATCGCGGGTTGGCCGCATTGCCCACGGAGAAGATCGGCTTGCTGCTCGACGAGACC
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                                                                        AsnGlyArg----
                                                                                                                                            SerAsnAsnAspIleThrGlyGlyAsnSerGlySer-----ProValPheAspLys 134
                                                                                                                                                                                  GTGTCCACCGGTGCTCCGGGTAAATACTTCTCCTCCGGACAG----
                                                                                                                                                                                                                    PheArgThrLysAsnTyrGlyArgTyrAlaGluAsnGlyGlnLeuHisIleAlaPheLeu
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US-09-815-242-7701

; Sequence 7701, Application US/09815242

; Patent No. US20020061569A1
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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 58 sGlyTyrGluProGlnAspGlyAlaTrp-----
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                                       GGTCGGCGCCCTGCTGGGGGGGCTTCCTGTGCCCAGGCGATGGCCTTC------
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Zyskind, Judith W.
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Percent Similarity:
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Sequence 1729, Application US/09974300; Patent No. US20020146721A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Berka, Randy M. APPLICANT: Clausen, Ib Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-10-06 PRIOR APPLICATION NUMBER: 60/279,526
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 8481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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346 GACCGTTATCGCCAGAAATCCCGATAAGTATGAGTGGTGGAACCTGATTACGATCAACAA 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73
                               56 -SerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThrThrGlyLy 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
                                                                                                             36 MetTyrProGlyArgAlaLeuProSerAspAlaAsnPheThrMetArgMetSerTyrGly 55
                                                                           GTCTTTAAGAAAAGAGCTCGGCCATCTGAAATCAATTAAAGACTACACGCCGATTCTGGC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nArgThrIleSerValAspIleArgTyr-----ValLeuPheMetIleAspLysTr 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATCGCCCGCCTGGCGGAGCGCGCCTCCTGGCCGCTTCGTGTTCCCGCGGCCGATGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGGCACCTGCTGGCGCCGATGCTGGAAGAGCAGCCACCGCGGTTCCCCGTTCGTCGCCTT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rGly------LysGlyValLeuGluLysGlnAspProLysSerAspGluPheAla--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----GAAGCCTTCGACAAGACCGCCAAGCTGATCGGCCTGGGCTATCCCGGTGGTCCGGA
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Matches:
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; SEQ ID NO 1841
; LENCTH: 1986
; TYPE: DNA
; ORGANISM: Bacillus 1
US-09-974-300-1841
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APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Ger
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT ETLING.DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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                                                                  436 AATAAAGGAAAGGTGATCATCACAAACCCCTTATAAAACAGCGTCAACCGGAACGATGGTC 495
                                     77
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                                                                                                                                                                                                                                                                                               18 ASnAlaTyrAlaIleGluLysGlyLysArgLeuPhePheAlaGlyLeuArgGlu-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTAAGCGCAACAGAACAGAACAACAACTGCCACAGTTATCGCTGCAGATAAAGGCAA 576
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                                  -----ValLeuGluLysGlnAspProLysSerAspGluPheAlaValGlnGluAsnIle 94
                                                                                                                                                                      TyrGlySerIleLysGlyTyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThrThr 73
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    LeuGluLysGlnAspProLysSerAspGluPheAlaValGlnGl

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Matches:
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APPLICANT: SWAISTROM, RONALD
TITLE OF INVENTION: ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR U
TITLE OF INVENTION: VACCINES
FILE REFERENCE: 01113.000103
CURRENT APPLICATION NUMBER: US/09/991,258
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 09/902,537
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-07
NUMBER: 09/902,537
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 1026
TYPE: DNA
TYPE: DNA
TYPE: DNA
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US-09-991-258-9
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Best Local Similarity:
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US-09-991-258-9
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451 ATGCATGTGGAAAGCAAAGATCGACAACGACGTTCTGGCCGCGCGTTAAGACGAAGAAAGCA 510
                                                                                                                                                           334 CCAGGCAAGAGACAGCGCATGGTCATGAAATTGGAATCTGACAAGACGTTCCCAATC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 ---LeuAlaPheAspGlyAsnTrpGluAlaMetSer 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               667 GAAGGCAAAGGC--
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                                                                             391 ATGTTGGAAGGGAAGATAAACGGCTACGCTTGTGTGGTCGGAGGGAAGTTATTCAGGCCG 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    721 CAATATACATTTGAAGGAAAAGAAAAGAAAATGGCT 756
                                                                                                                                                                                           38 ProGlyArg-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGTTTATTTCAAGCAATGACAAAAAATATGTTGCCCCATCCGACAATCGAAGCCGGAACC 666
                                      TyrHisThrThrGlyLys----
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Johnston, Robert
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Caley, Ian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keith, Paula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description of Artificial Sequence;
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24.54%
7.43%
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                                                                                                                                                                                             ---AlaLeuProSerAspAlaAsnPheThrMetArg 51
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Matches:
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                                    -GlyValLeuGluLysGlnAsp 82
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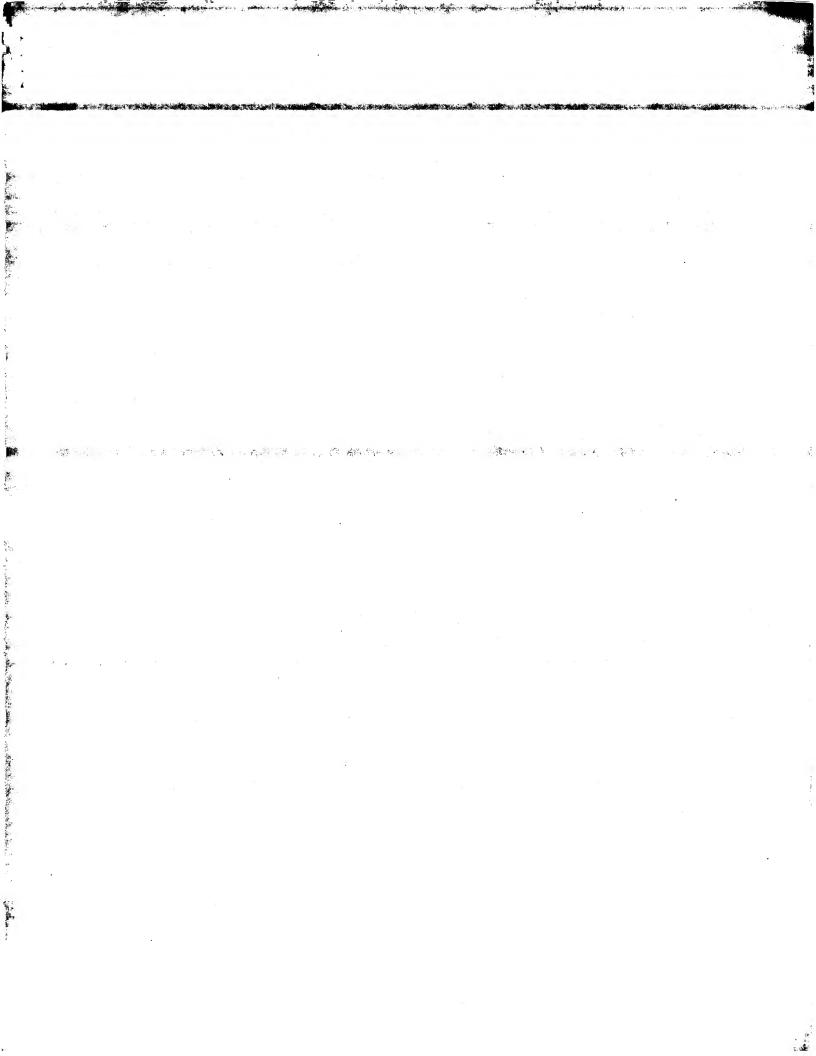
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                                                                                      US-10-008-355-2_COPY_522_712 (1-191)
                                                                                                                                             Percent Similarity:
Best Local Similarity:
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                                                                                                                                Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/991,258
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 09/902,537
PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/216,995 PRIOR FILING DATE: 2000-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE TITLE OF INVENTION: VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Olmsted, APPLICANT: Keith,
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 01113.0001U3
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                                                                                                                                                                                                                                               OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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                               909 CCAGGCAAGAGACAGCGCATGGTCATGAAATTGGAATCTGACAAGACGTTCCCAATC--- 965
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Conservative:
Mismatches:
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US-10-008-355-2_COPY_522_712 (1-191) x US-09-952-360-1 (1-14759)
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Best Local Similarity:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/661,887
PRIOR FILING DATE: 2000-09-14
NUMBER OF CENTRAL PRIOR FILING DATE: 2000-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Styrkarsdottir, Unnur
APPLICANT: Johannsdottir, Vala Drofn
TITLE OF INVENTION: Human Osteoporosis Gene
FILE REFERENCE: 2345.2009-01
CURRENT APPLICATION NUMBER: US/09/952,360
CURRENT FILING DATE: 2001-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (3639)...(3984)
NAME/KEY: CDS
LOCATION: (11757)...(1260)
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                                                               1259 AGCGCGAGCCGGGCGCAGCGCGGCGGCGGCGAGGACTCCGGCGGCGGCGACGGCGGCGGCGGCG
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                                                                                                    6 AlaAlaAlaArgAlaIleGlnAlaAspAlaMetAlaAsnAlaTyrAlaIleGlu-
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	355-2_COPY_522_712 (1-191) GluLvsGlvLvsArgLeu	Scores: 2 imilarity: 3 l Similarity: 2 ch: 7		GCGCCGTGGCGCGCCTCGCGGCTTTTAAAGGGGACGCCGCCTGCCGGCTCCCTCC

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                                                                               120 AsnAspIleThrGlyGlyAsnSerGlySerProValPheAspLysAsnGlyArgLeuIle 139
                                                                                                                                                                                304 TACGAAACTGAGAAGGTGCTTGAGGAACACGCGAGGAATCTCGGTGTCTGCATCCTTCGC 363
                     140 GlyLeuAlaPheAspGlyAsnTrpGluAlaMetSerGlyAspIleGluPheGlu 157
                                                                                                                                                                                                                                                                                                     259 TCTGCGCTTGACACGCGAGCCAATTTTACACTG------TTCATCCCCCAG 303
                                                                                                                                                                                                                                                                60 TyrGluProGlnAspGlyAlaTrpTyrAsnTyrHisThrThrGlyLysGlyValLeuGlu 79
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Search completed: December 21, 2002, 11:21:05
Job time: 71 secs



GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT: *
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT: *
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT: *
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT: *
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT: *
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358.463 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB	ength	DВ	ID	Description
ם	1003	100.0	712	23	AA015205	Porphyromonas ging
2	274	27.3	52	23	AA015206	Porphyromonas ging
w	90	9.0	711	17	AAR88649	Neisseria meningit
4	89.5	8.9	756	22	AAB95249	Human protein sequ
U	89.5	8.9	856	22	AAB94310	Human protein sequ
σ	89.5	8.9	866	22	AAM4 0262	Human polypeptide
7	89.5	8.9	923	22	AAM42048	Human polypeptide
8	89.5	8.9	3421	22	AAB84902	Chimeric protein f
9	86	8.6	1060	23	ABB53805	Lactococcus lactis
10	85.5	8.5	278	21	AAG40033	Arabidopsis thalia

Novel isolated dipeptidylpeptidase useful for identifying inhibitor of the dipeptidylpeptidase for protecting an animal from periodontal

4.5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
77	77	77.5	78	78	78	78	78	78	78	78	78	78.5	79	79.5	80	80	80	80	80	80.5	80.5	80.5	80.5	81	81	81.5	81.5	81.5	82			84	85.5	5
7.7	7.7			7.8		7.8	7.8	7.8	7.8	7.8				7.9						٠		٠	٠						8.2					
332	180	971	3432	870	846	803	781	684	509	215	52	498	571	389	392	357	344	344	336	4643	1317	532	532	283	283	309	254	240	870	360	201	537	323	321
21	23	19	21	22	21	21	21	22	22	17	23	21	18	23	17	13	18	17	13	22	22	18	17	23	21	23	22	22	21	23	22	18	21	21
AAY68962	AAU75485	AAW48896	ABB07037	AAB94408	AAG31211	AAG31212	AAG31213	AAM93433	AAM25688	AAR91044	AAO15207	AAY75500	AAW16399	ABB53562	AAR91034	AAR26842	AAW22218	AAR91033	AAR29644	ABB71609	ABG18723	AAW22219	AAR91035	AAU96101	AAY71478	ABP25673	AAU36684	AAU33855	AAB41742	ABP39512	AAG82591	AAW22220	AAG40031	AAG40032
ps2J p	S. aureus antigent	Candida albicans C	ise en	۳.		Arabidopsis thalia	Arabidopsis thalia	Human polypeptide,	Human protein sequ	V8 mature protease	Staphylococcus aur	Neisseria meningit		Lactococcus lactis	actosid	Protease from S. A	Protein encoded by	Beta-galactosidase	Protease from S. A	Drosophila melanoq	Novel human diagno	Protein encoded by	_	Ehrlichia canis p2	Ehrlichia canis im	Streptococcus poly		Staphylococcus aur	Human ORFX ORF1506	aphylococcus	S. epidermidis ope	0	thal	Arabidopsis thalia

ALIGNMENTS

RESULT 1 AAO15205 ID AAO15205 standard; XX AC AAO15205; XX XX	d; Protein; 712 AA.
	05-SEP-2002 (first entry) Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7).
	Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; gingivitis;
	identification; periodontal disease; gingivitis
OS Porphyromonas gingivalis.	ngivalis.
PN WO200238742-A2.	
PD 16-MAY-2002.	
PF 08-NOV-2001; 2001WO-US46782.	1WO-US46782.
XX PR 08-NOV-2000; 2000US-246827P	10US-246827P.
	(UYGE-) UNIV GEORGIA RES FOUND INC.
PI Travis J, Pote	Potempa JS, Banbula A, Bugno M;
DR WPI; 2002-490075/52. DR N-PSDB; AAL43635. XX	./52.
	Novel isolated dipeptidylpeptidase useful for identifying inhibithe dipeptidylpeptidase for protecting an animal from periodonta

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RESULT 2
AAO15206
               FINANCE PROPERTY OF THE PROPER
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Novel isolated dipeptidylpeptidase useful for identifying inhibitor of the dipeptidylpeptidase for protecting an animal from periodontal
                                                                                                 WPI; 2002-490075/52
                                                                                                                                                                                                                                                                            08-NOV-2000; 2000US-246827P
                                                                                                                                                                                                                                                                                                                                   08-NOV-2001; 2001WO-US46782
                                                                                                                                                                                                                                                                                                                                                                                                16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200238742-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           periodontitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dipeptidylpeptidase-7; DPP-7; enzyme; amidolytic cleavage; DPP-7 inhibitor identification; periodontal disease; gingi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porphyromonas gingivalis dipeptidylpeptidase-7 (DPP-7) C-terminal region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAO15206 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                  (UYGE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SKSVIAAARAIQADAMANAYAIEKGKRLFFAGLREMYPGRALPSDANFTMRMSYGSIKGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPQDGAWYNYHTTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CPRLIQELKLI 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191;
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                                                                                                                                                                                                               UNIV GEORGIA RES FOUND INC
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                                                                                                                                                        Potempa JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                712 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                        Banbula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1003; DB 23; Pred. No. 9.6e~101;
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                                                                                                                                                        P
                                                                                                                                                        Bugno M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gingivitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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RESULT 3
AAR88649
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Best Local
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           Jacobs E,
Millet MBJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The DPP-7 target peptide has an aliphatic or aromatic residue as a substituent on the alpha-carbon atom of the second amino acid from the N-terminal end. The DPP-1 protein and DNA sequences of the invention are useful for identifying a DPP-7 inhibitor. DPP-7 inhibitors are useful for reducing the growth of a bacterium and protecting an animal from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             periodontal disease caused by Porphyromonas gingivalis (e.g. gingivitis or periodontitis). The present amino acid sequence represents the C-terminal region of the Porphyromonas gingivalis dipeptidylpeptidase-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises the amino acid and coding sequence of the Porphyromonas gingivalis dipeptidylpeptidase<sup>7</sup> (PPP-7) enzyme. The DPP-7 enzyme has amidolytic activity for cleavage of a peptide bond between the second and third amino acids from the N-terminal end of a target peptide.
                                             (INMR ) PASTEUR ME
(TRGE ) TRANSGENE
                                                                                           31-MAY-1994;
                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferrin receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis BZ163 transferrin receptor Tbp2 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR88649 standard; Protein; 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease caused by Porphyromonas gingivalis
                                                                                                                      30-MAY-1995;
                                                                                                                                                 07-DEC-1995
                                                                                                                                                                            WO9533049-A2.
                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                       passive immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR88649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DPP-7) enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Fig 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFM 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFM 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity
52; Conserv
                                                               PASTEUR MERIEUX SERUMS
                                                                                                                                                                                                                                                                                                                                                                                                          meningitidis (strain BZ163).
                        Legrain M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                      95WO-FR00701.
                                                                                           94FR-0006594.
                                                                                                                                                                                                                                                                       /note= "N-terminal domain" 367..564
                                                                                                                                                                                                       /note= "C-terminal domain"
                                                                                                                                                                                                                                          /label= Domain_2
/note= "hinge domain"
                                                                                                                                                                                                                                                                                                                                                      /label= Tbp2_subunit
                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                          label= signal_peptide
                                                    SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tbp2 subunit; deletion mutant; vaccine,
                         Mazarin V,
                                                                                                                                                                                                                     Domain_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 274; DB 23; Pred. No. 1.7e-22;
                                                                 & VACCINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
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                                                                                                                                                                                                                                                                                                                                                                                                                                       IM2169; IM2394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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RESULT 4
AAB95249
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  ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domains (see features table); deletion mutants in which at least one of the domains is partially or totally deleted are claimed, provided that the first and second domains are not simultaneously partially or totally deleted. The positions of the 3 domains in BZ163 are defined by alignment with the IMZ169 sequence. The deletion mutant polypeptides of the invention can generate an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptide(s) for vaccination against Neisseria meningitidis group B - comprising deletion mutants of transferrin receptor Tbp2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT11244
                                                                                                                                                                                                                                                                                                 Human; primer;
                                                                                                                                                                                                                                                                                                                        Human protein sequence SEQ ID NO:17413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 82-87;
            Primer sets
                                                                                                                                   11-JAN-2000; 2000JP-0118776
02-MAY-2000; 2000JP-0183767
                                                                                                                                                             29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                          07-FEB-2001.
                                                                                                                                                                                                                                                  EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                   26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                            AAB95249;
                                                                                                                                                                                                                                                                                                                                                                                                   AAB95249 standard;
Primer sets for synthesizing full-length cDNAs defined in
                                                                                                (HELI-) HELIX RES INST.
                                                                                                                                                                                                 28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transferrin Tbp2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   607
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                                                                                                                                                                                                                                                                          sapiens
                                      2001-318749/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---GSWYGHIASSTSWSGNASDKEGGNRAEFTV------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSVIAAARAIQADAMANAYAIEKGKRLFFAGLREMYPGRALPSDANFTMRMSYGSIKGYE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1996-030562/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TAENRQEATFTIDGKIEGNGFSGT--AKTAELGFDLDQKNTTRTPKAYI 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNNDITGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PQDGAWYNY---HTTGKG-VLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFL 117
                                                              ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        response against N.meningitidis.
                                                          Isogai T,
, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence is that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                         2000JP-0241899
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                                                                                                                                                            99JP-0300253
                                                                                                                                                                         99JP-0248036
                                                                                                                                                                                                                                                                                                detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subunit.
                                                            Nishikawa
T, Wakama
                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.0%;
21.8%;
                                                              hikawa T,
Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Tbp2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 90;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the N.meningitidis strain BZ163 e Tbp2 polypeptide has three
polynucleotides, particularly the 5602 the specification, and for the detection
                                                                                                                                                                                                                                                                                                                                                                                                   Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                           Hayashi K,
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66;
                                                                        Saito
                                                            otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEGEKKITGTL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                            Yamamoto T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                565
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RESULT 5
AAB94310
ID AAB9
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Best Local
           29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention full-length cDNAs def:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                           07-FEB-2001
                                                                                                                                                                         EP1074617-A2
                                                                                                                                                                                                                                       Human; primer;
                                                                                                                                                                                                                                                                                                        26-JUN-2001
                                                                                                                                                                                                                                                                                                                                        AAB94310
                                                                                                                                                                                                                                                                                                                                                                    AAB94310 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     full-length cDNAs
                                                                                                           28-JUL-2000;
                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                       Human protein sequence SEQ ID NO:14779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGK------KSTN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYGVRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQLGEEPFS---YGYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYAIEKGKRLFFAGLREMYPGRALPSDA--NFTMRM----SYGSIKGYEPQDGAWYNYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGNDVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYG-RYAENGQLHIAFLSNNDITG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    t invention describes primer sets for synthesising 5602 h cDNAs defined in the specification. Where a primer set (a) an oligo-dT primer and an oligonuclectide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                756
           99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                           2000EP-0116126
                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention.
                                                                           99JP-0248036.
                                                                                                                                                                                                                                     detection; diagnosis; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                     entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SRFENYGDKFAE----
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ed. No. 1.5;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 756;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -NDVIGCFADFE
                                                                                                                                                                                                                                   gene therapy
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RESULT 6
AAM40262
ID AAM4
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XX AAM4
XX PUT 22-0
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XX HUMA
XX HUMA
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Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides. Particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH39893 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                        chemokinetic;
                                                        peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                         Human polypeptide SEQ ID NO 3407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3 -end sequence, where the oligonucleotide comprises at least 15 nucleotides and the comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID 14779; 2537pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                     Human; nootropic;
                                                                                                                                                                                                                                              AAM40262;
                                                                                                                                                                                                                                                                                   AAM40262 standard;
                     leukaemia
                                                                                                                                                                                                     22-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity es 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYG-RYAENGQLHIAFLSNNDITG----- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYGVRRGRYCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQLGEEPFS---YGYG 305
                                                                                                                                                                                                                                                                                                                                                                                    CGNDVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF
                                                                                                                                                                                                                                                                                                                                                                                                                          -GNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGK-----KSTN-----SRFENYGDKFAE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AYAIEKGKRLFFAGLREMYPGRALPSDA--NFTMRM-----SYGSIKGYEPQDGAWYNYH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
A
                                                                                              immunosuppressant; cytostatic; gene therapy;
s system; neuropathy; central nervous system;
                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nishikawa T, Ha
T, Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.9%; Score 89.5;
25.1%; Pred. No. 1
                                     drug
                                                                                                                                                                                                                                                                                   866
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A, Nagai K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saito K, Y, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----NDVIGCFADFE
                                                                                                                                                                                                                                                                                                                                                                                                                            170
                                                                                                                                                                                                                                                                                                                                                                                      383
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RESULT 7
AAM42048
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                                                                                                                                                                                                                         Query Match
Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous snjuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang
Wang
                                                                                                                                                                                                                                                                                                                                          Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
AAM42048 standard; Protein;
                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                     C.N.S disorders
Note: The sequen
                                                                                                                                                                                                                                                                                                         specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAI59418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao
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19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-)
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                                                                  337
                                                                                          125
                                                                                                                     306
                                                                                                                                                                       249
                                                                                                                                            72
                                                                                                                                                                                                19
                                                                                                                                                                                                                         Local Similarity
les 42; Conserv
                                                                CGNDVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF
                                                                              -GNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRY
                                                                                                                     GTGK--
                                                                                                                                 TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYG-RYAENGQLHIAFLSNNDITG------
                                                                                                                                                                      SYGVRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQLGEEPFS---YGYG 305
                                                                                                                                                                                                AYAIEKGKRLFFAGLREMYPGRALPSDA--NFTMRM-----SYGSIKGYEPQDGAWYNYH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                     sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 3407; 10078pp; English.
                                                                                                                                                                                                                                                                               866 AA;
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
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2000US-0693036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asundi V,
Wehrman T,
Goodrich R
                                                                                                                                                                                                                                                                                                                     data
                                                                                                                                                                                                                                    8.9%;
25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                    for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        system
                                                                                                                                                                                                                          22;
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                                                                                                                                                                                                                        Score 89.5; DI
Pred. No. 1.8;
22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen R,
Xu C,
                                                                                                                   -SRFENYGDKFAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        injuries
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Xue AJ,
lac RT;
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8
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Yang Y,
                                                                                                                                                                                                                          56;
                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                                                                                                                                                    part
                                                                                                                     NDVIGCEADEE 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ren F,
                                                                                                                                                                                                                                                      866;
                                                                                                                                                                                                                                                                                                                    of the printed
                                                                                                                                                                                                                          47;
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Best Local
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                                                                                                                                                                                                                         The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotactic/chemokinetic activity, heemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                    assays
C.N.S d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang
Wang
                                                                                                                                                               Sequence
                                                                                                                                                                                         specification.
                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; SEQ ID NO 6979; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-2000;
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19-JUL-2000;
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25-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human: nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; anyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leukaemia.
 363
                                                     306
                     72 TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYG-RYAENGQLHIAFLSNNDITG----- 124
                                                                                19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QA,
 GTGK-----KSTN----
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                                                  SYGVRRGRYCFEMKINEEISVKHLPSTEPDPHYVRIGWSLDSCSTQLGEEPFS---YGYG 362
                                                                            AYAIEKGKRLFFAGLREMYPGRALPSDA--NFTMRM-----SYGSIKGYEPQDGAWYNYH 71
                                                                                                                                                                                                   The sequence data for this patent did
                                                                                                                                                                                                                    disorders.
                                                                                                          l Similarity
42; Conserv
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Wang Z,
Zhou P,
                                                                                                                                                              923 AA;
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2000US-0552317.
2000US-0558042.
2000US-0620312.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-06633036.
                                                                                                          Conservative
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Wehrman T,
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                                                                                                                      8.9%;
25.1%;
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                                                                                                          22;
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, Xu C,
                                                                                                       Score 89.5; D
Pred. No. 2;
22; Mismatches
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 --SRFENYGDKFAE----
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Xu C, Xue AJ,.
Drmanac RT;
                                                                                                                                   DB
                                                                                                                                                                                                    not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qian XB,
. Yang Y,
                                                                                                                                  22;
                                                                                                        56;
                                                                                                                                                                                                   form
                                                                                                                                Length 923;
                                                                                                        Indels
                                                                                                                                                                                                   part
-NDVIGCFADFE
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Zhang J;
                                                                                                        47;
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                                                                                                     Gaps
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RESULT 8
AAB84902
ID AAB8
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                                                                                   Query Match
Best Local
                                                                     Matches
                                                                                                                                                                                    genome of the yellow fever virus a nucleotide sequence encoding a prN-E protein of a second, different flavivirus so that the prM-E protein of the second flavivirus is expressed. The chimeric live, infectious, attenuated virus is used to prepare medicaments for preventing or treating flavivirus infection in a patient. The yellow fever virus vector produces its gene product (tumor antigen or cytokine) in cells of the lymphoid or reticuloendothelial system or in a precursor of these systems in patients with cancer. Flaviviruses replicate in the cytoplasm of cells that the virus replication does not involve integration of the viral genome into the host cell. The present sequence represents a chimeric
 1552
                                                                                                                                                                                                                                                                                                                                                          The invention relates to a chimeric live, infectious, attenuated virus comprising a yellow fever virus with the nucleotide sequence encoding a prM-E protein deleted, truncated or mutated so that functional yellow fever virus prM-E protein is not expressed and also integrated into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 200-215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric live, infectious, attenuated yellow fever viruses used for preventing and treating diseases caused by flaviviruses have prM-E nucleotide sequence from a second, different flavivirus as functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chambers TJ, Monath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; virucide; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yellow fever virus; prM-E protein; flavivirus; chimeric; medicamen infection; tumor antigen; cytokine; lymphoid; reticuloendothelial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric protein from yellow fever virus and Japanese encephalitis virus.
                                                                                                                                       Sequence
                                                                                                                                                                       protein derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yellow fever prM-E is not expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-343953/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2000; 2000WO-US32821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200139802-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Flavivirus febricis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB84902 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ORAV-) ORAVAX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394
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                                   19
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 AFLVRNGKKL-----
                                 AYAIEKGKRLFFAGLREMYPGRALPSDANFTMRM-SYGSIKGYEPQDGAWYNYH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRY 170
                                                                     39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF83821.
                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encephalitis virus.
                                                                                                                                       3421 AA;
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0452638
                                                                                                                                                                     from yelllow fever virus and Japanese encephalitis virus
                                                                                8.9%;
25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΤP,
                                                                                                                                                                                                                                                                                                                                                                                                                                               232pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guirakhoo
--IPSWASVKEDLVAYG---GSWKLEGRWDGEEEVQLIA 1595
                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3421 AA
                                                                                   Score 89.5;
Pred. No. 14;
                                                                   Mismatches
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                                                                                                     DB
                                                                   46;
                                                                                                   22;
                                                                                                  Length 3421;
                                                                   Indels
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                                                                  Gaps
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72

-TTGKGVLEKODPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSP 130

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RESULT 9
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                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                             Matches
                                                                                                                                                                                                                                           production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                   The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB5300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1596
                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                        New nucleotide sequence useful in the identification or Lactococcus lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-043418/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bolotine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-2000; 2000FR-0004630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-APR-2000; 2000FR-0004630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FR2807446-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactococcus lactis protein dnaE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB53805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB53805 standard; Protein; 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactococcus lactis IL1403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAY-2002
                                                                                                                                                                                                                                                                                           invention helps research in lactic bacteria, particularly useful in the
                      154
                                            850
                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131
                                                                                       790
                                                                                                                                  743
                                                                                                                                               14 DAMANAYAIEKGKRLFFAGLREMYPGRALPSDANFT----MRMSYGSIKGYEPQDGAWYN 69
                                                                                                             70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVNRNGEVIGLYGNG---ILVGDNSFVSAISQT 1665
                     IEFEPDLQRTISVDIRYVLFMIDKWGQ 180
                                          DIFMASSGGGFAYHEAEDYSETEKYDFEKN--LLGIGVTPHPLQNLARRFEGNFTPLA-- 905
                                                                  DITGGNSGSPV-
                                                                                      ENOPYKOLADFVEKLPNNFHKKENILPLIQIGAFDYADSNRGKLAYNLADHANLLNYYSD
                                                                                                                                   DALENGFEIEK --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVPGKNVVNVQTKPS------LFKVRNGG---EIGAVAL-----DYPSGTSGSP 1635
                                                                                                           YHTTGKGVLEKQDPKSDEFAVQENILDL-----FRTKNYGRYAENGQLHIAFLS--NN 120
-QLVKNRRMTILVEINYIRTHRTKTGQ 931
                                                                                                                                                                                                                                                                                                                                                                                   6;
                                                                                                                                                                                45;
                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID No 507; 2504pp; French.
                                                                                                                                                                                                                          1060 AA;
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sorokine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                         8.6%;
21.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Renault P,
                                                                                                                                                                             31;
                                                                                                                                                                            Score 86; DB Pred. No. 6; 31; Mismatches
                                                                ----FDKNGRLIGLA-------FDGNWEAMSGD 153
                                                                                                                                 PSINLMKIGDFVKNKKIRLGLAHVQGISRDLAKWIV 789
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                                                                                                                                                                             73;
                                                                                                                                                                                                 Length 1060;
                                                                                                                                                                             Indels
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                                                                                      849
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AAG40033
01-JUN-1999
03-JUN-1999
04-JUN-1999
07-JUN-1999
08-JUN-1999
10-JUN-1999
                                                                                                                                                                  24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
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05-MAR-1999;
09-MAR-1999;
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07-MAY-1999
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06-MAY-1999
        18-JUN-1999;
18-JUN-1999;
                              16-JUN-1999;
17-JUN-1999;
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16-JUN-1999;
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01-APR-1999
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Вb
                    The invention relates to new mutant Staphylococcus aureus V8 proteases which have enzyme activity even under environmental conditions which protein denaturation. The mutants are based on 3 truncated V8 proteases lacking 48 (AAW22218), 56 (AAW22219) or 53 (AAW22220) amino caids from the C-terminal of the wild type protease. The mutants also contain amino acid substitutions, especially D44E, N71S and/or R147K. The protein sequence shown here represents a chimaeric protein comprising a truncated Staphylococcus aureus V8 protease lacking the preparate of the E. coli beta-galactosidase. Also included downstream of the V8 protease fragment; is a second R6 linker and a fragment of the Caminoglucoside 3'-phosphotransferase protein. The chimaeric sequence was generated by restriction digestion and ligation from the V8RPT(-) CC sequence (see AAW22218) by using a natural EcoRV site which removed a CC further 8 amino acid from the C-terminus. This truncated V8 protease, according to the concentration of protein denaturant e.g. 5 M urea.
                                                                                                                                                                                                                                                                                              Claim 8; Page 19-20; 42pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric - Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteolytic activity; fusion protein; beta-galactosidase; urea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutant; Staphylococcus aureus; V8 protease; enzyme; denaturation; pri
truncation; wild type; PCR; polymerase chain reaction; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein encoded by pV8F construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW22220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW22220 standard; Protein; 537 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                      (SUNR ) SUNTORY LTD
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                                                                                                                                                                                                                                                                                                                                                                                                        Yabuta M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                              denaturation
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/note= "E. coli beta-galactosidase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "truncated S. aureus V8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "R6 linker sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "aminoglucoside 3'-phosphotransferase'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "R6 linker sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protease'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer;
                                                                                                                                 of
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Sequence

Query Match Best Local Similarity

8.3%; 24.5%;

Score Pred.

No. DB 1.1; 22;

Length 201;

Sequence

201 AA;

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RESULT 14
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Best Local
                                                                                                             (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                  AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding useful for vaccinating
                           N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4464.
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 18; Page 606; 2188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-316495/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kimmerly WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus epidermidis SR1 strain; infection; diagnosis;

    epidermidis open reading frame protein sequence SEQ ID NO:2276.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 KWGQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFMI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RWGR 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
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                                                                                                                                                                                      ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed
                                                                                                                           Sequence
                                                                                                                                                                         N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID 4357; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-381255/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6380370-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4357.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP39512;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENO-) GENOME THERAPEUTICS CORP.
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                           57 IKGYEPQDGAWYNYHTTGKGVLEKQDPKSDEFAVQENILDLERT-KNY-----GRYAEN 109
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                                                                               Local Similarity
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MKGAHPMKNIKKPEDLKGKSLLKEYDLTGEEF---EGLIDFAMTLKKYKQQGTPHRYLEG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQL------HIAFLSNNDITGGNSGSPVFDKNGRLIGLAFDG 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKGYEPQDGAWYNYHTTGKGVLEKQDPKSDEFAVQENILDLFRT-KNY-----GRYAEN 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKGAHPMKNIKKPFDLKGKSLLKEYDLTGEEF --- EGLIDFAMTLKKYKQQGTPHRYLEG 57
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                                                                                                                                                                                                                                                                                                                                                                                                                            ABN92057.
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97US-064964P.
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Search completed: December 20, Job time: 79 secs

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Database
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427.5
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1: /cgn2_6/ptodata/2/pubpaa/U
2: /cgn2_6/ptodata/2/pubpaa/U
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5: /cgn2_6/ptodata/2/pubpaa/U
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10: /cgn2_6/ptodata/2/pubpaa/U
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 summaries
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// cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
// cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: *
// cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: *
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US-09-815-242-12277
12 US-10-062-624-4
10 US-09-815-242-1217
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10 US-09-911-258-10
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10 US-09-918-532-54
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             Sequence 2, Appli
Sequence 9, Appli
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Sequence 7, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 5351, Ap
Sequence 12277, A
Sequence 12277, A
Sequence 4, Appli
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Sequence 10, Appli
Sequence 11, Appli
Sequence 14, Appli
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Sequence 44,
Sequence 11
Sequence 5,
Sequence 24,
Sequence 6,
Sequence 4,
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US-09-925-297-718	US-09-886-468-21	US-09-815-242-11617	US-09-815-242-13866	US-10-059-964-2	US-10-062-624-9	US-09-846-808-19	US-10-062-994-18	US-10-062-994-18	US-09-925-299-923	US-09-815-242-12894	US-09-815-242-5859	US-10-095-139-8	US-09-344-882-16	US-09-971-536-62	US-09-829-094B-2	US-09-925-299-911	US-09-815-242-10274	US-09-815-242-11798	US-09-757-781-2	US-09-815-242-13511	US-10-135-322-10	US-09-925-300-1538	US-10-059-964-40	US-09-987-107-46	US-10-062-994-4
Sequence 718, App	Sequence 21, Appl	Sequence 11617, A	Sequence 13866, A	Sequence 2, Appli		Sequence 19, Appl	18,	Sequence 18, Appl	Sequence 923, App	Sequence 12894, A	59,	Sequence 8, Appli	Sequence 16, Appl		Sequence 2, Appli	Sequence 911, App	Sequence 10274, A	117	Sequence 2, Appli	Sequence 13511, A	Sequence 10, Appl	Sequence 1538, Ap	Sequence 40, Appl	Sequence 46, Appl	Sequence 4, Appli

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US-10-008-355-2
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CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10008355
Patent No. US30020164759A1
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potenpa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And
FILE REFERENCE: 235.00440101
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 191; Conserv
                                                                                                                                                                                       702
                              181 CPRLIQELKLI 191
                                                           61
                                                                                                                                           EPQDGAWYNYHTTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNN 120
CPRLIQELKLI 712
                                                                                                                           EPQDGAWYNYHTTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNN
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Pred. No. 3.7e-96;
D; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Aggieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Mei
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
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: LENGTH: 720

: TYPE: PRT

: ORGANISM: Porphyromonas gingivalis

US-10-008-355-9
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US-10-008-355-9
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TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-008-355-8
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
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                                                                                                                                                                                Query Match 42.6%; Score 427.5; DB 9; Best Local Similarity 47.4%; Pred. No. 1.9e-36; Matches 81; Conservative 34; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/10008355
Patent No. US20020164759A1
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Best Local Similarity 100.0%; Pred. No. 3.2e-89;
Matches 178; Conservative 0; Mismatches 0;
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APPLICANT: Potempa, Jan S
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases and Methods Of Use
TILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
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                                          82 DPKSDEFAVQENILDLFRTKNYGRYAE-NGQLHIAFLSNNDITGGNSGSPVFDKNGRLIG 140
                                                                                                                                     22 IEKGKRLFFAGLREMYPGRALPSDANFTMRMSYGSIKGYEPQDGAWYNYHTTGKGVLEKQ 81
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DPDNWEFVVDPKLKAVYERKDFGRYADRSGRMPVAFCATTHTTGGNSGSPVMNANGELIG
                                                                                          ILRAQRTYIAGLLEMDGDQDQFPDANLTLRFTYGQVKGYSPRDNYYYGHQTTLDGVMEKE 608
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; TYPE: PRT
; ORGANIZSM: XY1ella fastidiosa
US-10-008-355-7
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                                                                                                   ; SEQ ID NO 3
; LENGTH: 52
; TYPE: PRT
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APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agniesska
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local Similarity
Matches 74; Conserv
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                     Query Match
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Best Local Similarity
                                                                                                                                                                             APPLICANT: Travis, James
APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
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CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
                                                                                                                                                                 SOFTWARE: PatentIn version 3.0
                                                                            ORGANISM: Porphyromonas gingivalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QELKL 190
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27.3%;
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Pred. No. 9.5e-27;
0; Mismatches 53
Score 274; DB 9;
Pred. No. 5.1e-22;
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                     Length 52;
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: LENGTH: 732

: TYPE: PRT

: ORGANISM: Shewanella putrefaciens

US-10-008-355-6
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                                             ; ORGANISM: Shewanella putrefaciens US-10-008-355-5
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                                                                                  SEQ ID NO 5
LENGTH: 734
TYPE: PRT
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Best Local Similarity
Matches 67; Conserv
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Patent No. US20020164759A1
  Query Match
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                                                                                                                                                                                                                                                                     APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Diepetidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Potempa, Jan S
APPLICANT: Banbula, Agnieszka
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipettidylpeptidases And Methods Of Use
FILE REFERENCE: 235 00440101
CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/246,827
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
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                                                                                                                                              SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/008,355
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Travis, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Travis, James APPLICANT: Potempa, Jan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMSGDIEFEPDLORTISVDIRYVLFMIDKWGQCPRLIQELKLI 191
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  25.5%;
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  Score 255.5;
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                                                                                                                                                                                                                               Query Match
Best Local Similarity 23.0
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5351
LENGTH: 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/815, CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
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213 VKNDDNRNAYG--VYFTPEIKKFIAENI 238
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                                                                                                                                                               108 YPGKEDVSVIQVEERAIERGPKGENENDNVTPFKYAAGAKAGDRIKVIGYPHPYKNKYVL 167
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                                                                                                                    91 QENILDLFRTKN----YGRYAENGQLHIAFLSNNDITGGNSGSPVFDKNGRLIGLAF--- 143
                                                                                                                                                                                                       37 YPGRALPSDANFTMRMSYGSIKGYEPQDGAW-YNYHTTGKG-----VLEKQDPKSDEFAV 90
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                                       ---DGNWEAMSGDIEFEPDLQRTISVDI
                                                                                HESTGPVMSVEGSSIVYSAHTES----
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                                                                                                                                                                                                                                                8.1%; score 81.5; DB 10;
23.0%; Pred. No. 0.36;
tive 22; Mismatches 59;
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                                                                                   -GNSGSPVLNSNNELIGIHFASD 212
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RESULT 10
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                                                                                                     GENERAL INFORMATION:
APPLICANT: Walker, David H.
APPLICANT: McBride, Jere W.
APPLICANT: Yu, Xue-Jie
TITLE OF INVENTION: Homologous 28-Kilodalton Immunodominant Protein
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
FILE REFERENCE: D61520172/D1
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SEQ ID NO 12277
LENGTH: 254
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                                                                                                                                                                                                                                                                    Sequence 4, Application US/10062624 Patent No. US20020115840A1
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                    PRIOR APPLICATION NUMBER: 09/660,587 PRIOR FILING DATE: 2000-09-12
                                                                CURRENT APPLICATION NUMBER: US/10/062,624
CURRENT FILING DATE: 2002-01-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Identification of Essential Genes in
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NUMBER OF SEQ
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FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
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Zyskind, Judith W.
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ID NOS: 46
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23.0%;
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Pred. No. 0.38;
2; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GNSGSPVLNSNNELIGIHFASD 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 254;
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; OTHER INFORMATION: amino acid sequence of p28-5 protein
US-10-062-624-4
                                                                                                                                                                                                                                                                                           US-09-767-041-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Staphylococcus aureus US-10-008-355-4
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US-10-008-355-4
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Best Local Similarity
Matches 16; Consert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potemp, Jan S
APPLICANT: Banbula, Agnieszka
TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
FILE REFERENCE: 235.00440101
                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Smith, I
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 4
LENGTH: 283
                                                                                                                                                                                                                                                   Sequence 21, Application US/09767041 Patent No. US20020055168A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 43; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US Patent No. US20020164759A1
                                                                                           CURRENT APPLICATION NUMBER: US/09/767,041
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: PCT/NL99/00460
PRIOR FILING DATE: 1999-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/008,355
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/246,827
                   PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
                                                       PRIOR APPLICATION NUMBER: EP9
PRIOR FILING DATE: 1998-07-22
                                                                                                                                                                             FILE REFERENCE:
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TYPE: PRT
NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                         123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 VYLINEGLLNISFMTNICYETASKNIPLSPYICAGIGTDL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 VFDKNGRLIGLAFDGN--WEAMSGDIEFEPDLQRTISVDI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 EKKKTTVVYGLKENWAGDAISSQSPDDNFTIRNYSFKYASNKFLGFAVAIG-----YSIG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 EKGKRLFFAGLREMYPGRALPS---DANFTMR---MSYGSIK--GYEPQDGAWYNYHTTG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 KGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSP---- 130
                                                                                                                                                                                                                                                                                                                                                                     1 TGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDIHF 51
                                                                                                                                                                                                               Smith, Hilda
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                             2183-4726
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26.9%;
                       1998-07-22
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                                                                           EP98202465.5
                                         EP98202467.1
                                                                                                                 PCT/NL99/00460
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Pred. No. 0.11
13; Mismatches
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Pred. No. 0.5;
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NAME/KEY: misc_feature

OTHER INFORMATION: CPS2J
US-09-767-041-21
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Best Local Similarity 25.4%;
Matches 31; Conservative
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SEQ ID NO 21
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                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence; No. US20020141975Ale OTHER INFORMATION: synthetic construct
-09-991-258-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Olmsted, APPLICANT: Keith, I APPLICANT: Dryga,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/991,258
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 09/902,537
PRIOR FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/216,995 PRIOR FILING DATE: 2000-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 01113.0001U3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE TITLE OF INVENTION: VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                 LENGTH: 342
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptococcus suis
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                                        171 SKYDLEYADVPQNMRADTFKYTHEKPQGYYSWHHGAVQYENGRFTV---PKGVGAKGDSG 227
                                                                                                                           112
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                                                                              83 PKSD-EFA-VQENI-LDLFR---TKNYGRYA-----ENGQLHIAFLSNNDITGGNSG 128
                                                                                                                                                           38 PGR-----ALPSDANFTMRMSYGSIKGYEPQDGA--WYNYHTTGK------GVLEKQD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 DSDDIVDGNIVESLYTCLKENDSDLSGGLLA-TFDGNYQ------ESELQK-CQIDLE 138
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                                                                                                                                                                                                                          Local Similarity 24.5%;
                                                                                                                    PGKRORMVMKLESDKTFPI-MLEGKINGYACVVGGKLFRPMHVEGKIDNDVLAALKTKKA 170
SPVFDKNGRLIGLAFDG-----NWEAMSGDIEFEPD 159
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o. US20020141975A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Davis, Nancy
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                                                                                                                                                                                                                          7.4%; Score 74.5;
24.5%; Pred. No. 3;
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                                                                                                                                                                                                     Mismatches
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            APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION UMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/21,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26
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CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: DK PA2001 00057
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DK PA2000 01682
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
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                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11154, Applicatio Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 42;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GRAVERSEN, Jonas
APPLICANT: MOESTRUP, SOIGN
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA
                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                    APPLICANT:
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 SYTSTFSKLREQLGPYTQEFWDNLEKETE---GLRQEMSKDLEEV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 SGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYV 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 KRLFFAGLREMYPGRALPSDAN------FTMRMSYGSIKGY---EPQDGAWYNYHTTG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                  Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                           Ohlsen, Kari L.
Zyskind, Judith W.
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Gaps

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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2001-02-16
PRIOR PELLING DATE:
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Result
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            Pred. No. is the number of results predicted by chance to have a score greater than or, equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1

2: /cgn2_6/ptodata/1

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4: /cgn2_6/ptodata/1

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            /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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US-08-91-357-3
US-08-968-633-3
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Sequence 435;
Sequence 3, 1
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| Query Ma<br>Best Loc<br>Matches      | RESULT 1 US-08-657-11 US-08-657-11 Sequence Patent No GENERAL PITLE APPLICA AP | 20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>20<br>2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
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| tch<br>al Simi<br>18;                | -192 -192 -192 -192 -192 -192 -192 -192                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 7 77722.555<br>1 7722.5555<br>1 7722.55555<br>1 7725.5555555555555555555555555555555555                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| llarity<br>Conserva                  | 192-15 115, Application US 0. 5747321 CANT: VABUTA, MASA CANT: VABUTA, MASA CANT: OHSUYE, Kazu OF INVENTION: MUT OF INVENTION: PRO R OF SEQUENCES: 15 SPONDENCE ADDRESS: SPONDENCE ADDRESS: ETE: P.O. Box 1404 Y: Alexandria TE: Virginia NTRY: United State : 22313-1404 TER READABLE FORM: TUM TYPE: Floppy FATING SYSTEM: PC- TWARE: PATENTION DATA LICATION NUMBER: UNING DATE: 02-JUN-1 SSIFICATION: 45 APPLICATION DATA. LICATION NUMBER: 02-JUN-1 ING DATE: 02-JUN-1 ING DATE: 02-JUN-1 ING DATE: 03-JUN-1 ING DATE: | 7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| 8.4%;<br>28.1%;<br>tive 1            | /086 /086 /086 /086 /086 /086 /086 /086                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 37922 3 3 2 4 4 4 4 4 5 5 6 6 9 1 1 2 2 2 3 3 4 4 4 4 5 6 9 1 2 2 4 4 5 6 9 6 9 6 9 6 9 6 9 6 9 6 9 6 9 6 9 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| Score<br>Pred.<br>6; Mis             | 192<br>APHYL<br>-DOS<br>#1.0,<br>0086                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | US-08-44 US-08-48 US-08-48 US-08-49 US-08-47 US-08-47 US-08-47 US-08-47 US-08-48 US-08-48 US-08-63 US-08-63 US-08-63 US-08-63                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 84; DB 1;<br>No. 0.92;<br>smatches 2 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 08-449-733-2 08-867-921-62 08-867-921-62 08-867-890A-98 08-478-435-98 08-478-473-98 08-474-671-98 08-483-577A-98 08-483-577A-98 08-483-5218-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98 08-637-654-98                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
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| 537;<br>:ls 6;                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Sequence                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4357
LENGTH: 360
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 US-08-491-357-3
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 ; TYPE: PRT; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4357
 US-09-134-001C-4357
 GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
 Sequence 3, Applic Patent No. 5716782
 Query Match
Best Local
 Patent No. 6380370
 Matches
 Sequence
 GENERAL INFORMATION:
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
 ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
 APPLICANT: Estojak, JOAnne
TITLE OF INVENTION: NUCLEIC
TITLE OF INVENTION: MEDIATO
TITLE OF INVENTION: ALTERAT
 APPLICANT:
 APPLICANT:
 349 RWGR 352
 146 NWEAMSGDIEFEPDLORTI 164
 110 GQL-----
 57 IKGYEPQDGAWYNYHTTGKGVLEKQDPKSDEFAVQENILDLFRT-KNY-----GRYAEN 109
 APPLICATION NUMBER:
 COUNTRY:
 STATE:
 ADDRESSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street Suite 720
 77 KNIALLFEKTSTRTRAAFTVASIDLGAHPEFLGKNDIQLGKKES--VEDTAKVLGRMFDG 134
 20 MKGAHPMKNIKKPFDLKGKSLLKEYDLTGEEF---EGLIDFAMTLKKYKQQGTPHRYLEG 76
 Match 8.3%;
Local Similarity 24.5%;
 KWGQ 180
 | TGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDIHFELRLYRRHH 348
 -----IEFRGFSQKTV 145
 4357
 34;
 Philadelphia
 Application US/08491357
 PA
 USA
 Law, Susan
 Golemis, Erica A.
 Conservative
 Application US/09134001C
 NUCLEIC ACID MOLECULE MEDIATOR PROTEIN THAT
 ALTERATIONS
US/08/491,357
 15; Mismatches
 Score 83; DB 4
Pred. No. 0.66;
 --HIAFLSNNDITGGNSGSPVFDKNGRLIGLAFDG 145
 Version #1.30
 DB 4; Length 360;
 ENCODING A SIGNAL INDUCES CELLULAR MORPHOLOGICAL
 46; Indels
 44;
 Gaps
 6;
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 Query Match
Best Local Similarity
"~*~hes 43; Conserv?
 US-08-968-633-3
 ; ANTI-SENSE:
US-08-491-357-3
 sequence 3, Application US/08968633
Patent No. 6100384
 TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 563-4100
TELEPAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 3:
 GENERAL INFORMATION:
 APPLICANT:
APPLICANT:
 ATTORNEY, AGENT INFORMATION:
NAME: Reed, Janet E.
PERITSTRATION NUMBER: 36,252
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 SEQUENCE CHARACTERISTICS:
LENGTH: 872 amino acids
 ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION UNBER: 36,252
TELECOMMUNICATION INFORMATION:
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
 TITLE OF INVENTION:
TITLE OF INVENTION:
 MOLECULE TYPE:
 PRIOR APPLICATION DATA:
 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
 HYPOTHETICAL:
 688 GNIVRQGK-----GQLELQQLKQFERLEQEVSRPIDHDLANWTPAQPLVP--GRTGGL 738
 580 TLVACSRAVPEDAKQLASFLHGNASLLFRRTKAPGPGPEGSSSLHLNPTDKASSIQSRPL 639
 COUNTRY: USA
ZIP: 19103-2307
 STREET: 1601 Market
CITY: Philadelphia
 43
 CLASSIFICATION:
 STATE:
 STRANDEDNESS: not relevant TOPOLOGY: not relevant
 TYPE: amino acid
STRANDEDNESS: not
 CLASSIFICATION:
 APPLICATION NUMBER:
 FILING DATE:
 APPLICATION NUMBER: US/08/968,633
 ADDRESSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street Suite 720
 FRTKNYGRYAENGQLHIAFLS-----
 PSPPKFT---SQDSPDGQYENSEGGWMEDYDYVHLQGKEEFEK-----TQKELLEK 687
 PSDANFTMRMSYGSIKG-YEPQDGAW---YNY-HTTGKGVLEKQDPKSDEFAVQENILDL 97
 PΑ
 Estojak, JoAnne
 NO
O
: (215) 563-41
(215) 563-4044
 Law,
 Golemis,
 Conservative
 . protein
 Susan
 8.2%;
 NUCLEIC ACID MOLECULE ENCODING A SIGNAL MEDIATOR PROTEIN THAT INDUCES CELLULAR MORPHOLOGICAL ALTERATIONS
 Erica A.
 US/08/491,357
 18;
 Score 82; DB Pred. No. 3.1;
 Mismatches
 ----NNDITGGNSGSPVFDKNGRLIGL 141
 60;
 Length 872;
 Indels
 56;
 Gaps
 9
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

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LENGTH:

872 amino acids

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 US-09-196-466-3
 RESULT 5
 В
 ; ANTI-SENSE: NO US-08-968-633-3
 Sequence 3 Patent No.
 Query Match
 Matches
 GENERAL INFORMATION:
 TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
 TELEFAX: (215) 563-4044
NFORMATION FOR SEQ ID NO: 3:
 TYPE: amino acid
STRANDEDNESS: NO. 6100384 Relevant
TOPOLOGY: No. 6100384 Relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
 ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
 COMPUTER READABLE FORM,
MEDIUM TYPE: Floppy disk
 APPLICANT:
 PRIOR APPLICATION DATA; APPLICATION NUMBER: 08/491,357
 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
 CORRESPONDENCE ADDRESS
 APPLICANT:
 MOLECULE TYPE:
 SEQUENCE CHARACTERISTICS:
LENGTH: 872 amino acids
 HYPOTHETICAL:
 COUNTRY: USA
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 580 TLVACSRAVPEDAKQLASFLHGNASLLFRRTKAPGPGPEGSSSLHLNPTDKASSIQSRPL 639
 688 GNIVRQGK----GQLELQQLKQFERLEQEVSRPIDHDLANWTPAQPLVP--GRTGGL 738
 640 PSPPKET---SQDSPDGQYENSEGGWMEDYDYVHLQGKEEFEK-----TQKELLEK 687
 43 PSDANFTMRMSYGSIKG-YEPQDGAW---YNY-HTTGKGVLEKQDPKSDEFAVQENILDL 97
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 STATE:
 STREET:
 ADDRESSEE:
 STRANDEDNESS: not relevant TOPOLOGY: not relevant
 CLASSIFICATION:
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 Match 8.2%; Score 82; DB Local Similarity 24.3%; Pred. No. 3.1;
 FILING DATE:
 FRTKNYGRYAENGQLHIAFLS------NNDITGGNSGSPVFDKNGRLIGL 141
 3, Application US/09196466
 Philadelphia
 amino acid
 E: Dann, Dorfman, Herrell and Skillman 1601 Market Street Suite 720
 ESTOJAk, JOANNE
ESTOJAK, JOANNE
VENTION: NÜCLEIC ACID MOLECULE ENCODING A SIGNAL
VENTION: MÉDIATOR PROTEIN THAT INDUCES CELLULAR MORPHOLOGICAL
VENTION: ALTERATIONS
 Golemis, Erica A.
 Conservative
 Law, Susan
protein
NO
 US/09/196,466
 18; Mismatches
 DB 3; Length 872,
 60; Indels
 56;
 Gaps
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PSDANFTMRMSYGSIKG-YEPQDGAW---YNY-HTTGKGVLEKQDPKSDEFAVQENILDL 97

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 Query Match
Best Local Similarity
Matches 43; Conserve
 ; ANTI-SENSE: US-09-196-466-3
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 PCT-US96-10823_3
 PCT-US96-10823-3
 Sequence 3, Application PC/TUS9610823 GENERAL INFORMATION:
 Query Match
Best Local Similarity
 Matches
 TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
 HYPOTHETICAL:
ANTI-SENSE:
 MOLECULE TYPE:
 TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 563-4100
 CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION:
TITLE OF INVENTION:
 APPLICANT:
 APPLICANT:
 APPLICANT:
 NUMBER OF SEQUENCES:
580 TLVACSRAVPEDAKQLASFLHGNASLLFRRTKAPGPGPEGSSSLHLNPTDKASSIQSRPL 639
 688 GNIVRQGK----GQLELQQLKQFERLEQEVSRPIDHDLANWTPAQPLVP--GRTGGL 738
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 STREET:
CITY: F
 REGISTRATION NUMBER:
 FILING DATE:
 COUNTRY:
 98 FRTKNYGRYAENGQLHIAFLS------NNDITGGNSGSPVFDKNGRLIGL 141
 43 PSDANFTMRMSYGSIKG-YEPQDGAW---YNY-HTTGKGVLEKQDPKSDEFAVQENILDL 97
 STRANDEDNESS: not relevant TOPOLOGY: not relevant
 TYPE: amino acid
 APPLICATION NUMBER:
 ZIP: 19103-2307
 ADDRESSEE:
 3 SVIAAARAIQADAMANAYAIEKGKRLFFAGLREMYPG------
 LENGTH:
 PSPPKFT---SQDSPDGQYENSEGGWMEDYDYVHLQGKEEFEK-----TQKELLEK 687
 Philadelphia
 PΑ
 872 amino acids
 1601
 USA
 Estojak, JoAnne
 Golemis,
 Conservative
 Conservative
 NO
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 Dann, Dorfman, Herrell and
01 Market Street Suite 720
 NO
 protein
 Susan
 8.2%;
 8.2%; Score 82; DB 24.3%; Pred. No. 3.1;
 Erica A.
 MEDIATOR PROTEIN THAT INDUCES CELLULAR MORPHOLOGICAL ALTERATIONS
 NUCLEIC ACID MOLECULE ENCODING A SIGNAL
 PCT/US96/10823
 36,252
 18;
 18; Mismatches
 Score 82;
Pred. No.
 Mismatches
 Version #1.30
 w
 DB 3;
 DB 5;
 Skillman
 60;
 60; Indels
 Length 872;
 Length 872;
 Indels
 ----RAL 42
 56;
 56;
 Gaps
 Gaps
 9;
 9
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APPLICANT: W. KOBride, Jere W.
APPLICANT: Yu, Xue-Jie
TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
FILE REFERENCE: D6152CIP
CURRENT APPLICATION NUMBER: US/09/261,358A
CURRENT FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: 09/201,458
PRIOR FILING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 4
LENGTH: 283
TYPE: PRT
ORGANISM: Ehrlichia canis
 CURRENT APPLICATION NUMBER: US/09/660,587
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 09/261,358
PRIOR FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 4
FEATURE: PRT
ORGANISM: Ehrlichia canis
; FEATURE:
; OTHER INFORMATION: amino acid sequence of ECa28SA2 protein
US-09-261-358A-4
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 US-09-261-358A-4
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 ; OTHER INFORMATION: amino acid sequence of p28-5 protein US-09-660-587-4
 US-09-660-587-4
 GENERAL INFORMATION:
APPLICANT: Walker, David H.
APPLICANT: McBride, Jere W.
APPLICANT: Yu, Xue-Jie
 Sequence 4, Application US/09261358A Patent No. 6403780
 GENERAL INFORMATION:
 Sequence 4, Application US/09660587 Patent No. 6392023
 Query Match
 Matches
 APPLICANT: McBride, Jere W.
APPLICANT: Yu, Xue-Jie
TITLE OF INVENTION: Homologous 28-kilodalton Immunodominant Protein
TITLE OF INVENTION: Genes of Ehrlichia canis and Uses Thereof
FILE REFERENCE: D6152CIP2
 APPLICANT:
 162 VYLINEGLLNISFMTNICYETASKNIPLSPYICAGIGTDL 201
 131 VFDKNGRLIGLAFDGN--WEAMSGDIEFEPDLQRTISVDI 168
 113 SPRIE-----VEMSYEAFDVKNPGDNYKNGAYRYCALSHQDDADDDMTSATDKF 161
 688 GNIVRQGK----GQLELQQLKQFERLEQEVSRPIDHDLANWTPAQPLVP--GRTGGL 738
 75
 58
 23 EKGKRLFFAGLREMYPGRALPS---DANFTMR---MSYGSIK--GYEPQDGAWYNYHTTG 74
 Match 8.1%; Score 81; DB 4; Length 283; Local Similarity 26.9%; Pred. No. 0.77; es 43; Conservative 20; Mismatches 67; Indels
 KGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSP---- 130
 PSPPKFT---SQDSPDGQYENSEGGWMEDYDYVHLQGKEEFEK-----TQKELLEK 687
 FRTKNYGRYAENGQLHIAFLS----
 Walker, David H.
 -NNDITGGNSGSPVFDKNGRLIGL 141
 30;
 Gaps
 7;
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 ; MOLECULE TYPE: protein US-08-657-192-9
 RESULT 9
US-08-657-192-9
 Query Match
Best Local S
Matches 18
 Query Match
Best Local S
Matches 43
 Sequence 9, Applic
Patent No. 5747321
 GENERAL INFORMATION:
APPLICANT: YABUTA, Masayuki
APPLICANT: OHSUYE, Kazuhiro
 TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO:
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-170086

FILING DATE: 02-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Meuth, Donna M.

REGISTRATION NUMBER: 36,607

REFERENCE/DOCKET NUMBER: 001560-2
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,192
FILING DATE: 03-JUN-1996
 SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
 CORRESPONDENCE ADDRESS: ADDRESSEE: BURNS, DO
 TITLE OF INVENTION:
 NUMBER OF SEQUENCES:
289 TGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDRLYRRHHRWGR 347
 123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLF-MIDKWGQ 180
 162 VYLINEGLLNISFMTNICYETASKNIPLSPYICAGIGTDL 201
 131 VFDKNGRLIGLAFDGN--WEAMSGDIEFEPDLQRTISVDI 168
 Local Similarity les 18; Conserv
 CITY: Alexandria
STATE: Virginia
 TOPOLOGY:
 STRANDEDNESS:
 COUNTRY: United ZIP: 22313-1404
 75 KGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSP---- 130
 23 EKGKRLFFAGLREMYPGRALPS---DANFTMR---MSYGSIK--GYEPQDGAWYNYHTTG 74
 TYPE: amino acid
 TELEPHONE:
 CLASSIFICATION:
 STREET:
 Local Similarity
 EKKKTTVVYGLKENWAGDAISSQSPDDNFTIRNYSFKYASNKFLGFAVAIG-----YSIG 112
 43;
 Virginia
 Application US/08657192
 P.O. Box 1404
 United States
 Conservative
 8.0%; Score 80.5; DB 1; Length 532; llarity 30.5%; Pred. No. 2.2; Conservative 15; Mismatches 25; Indels
 linear
 single
 8.1%; Score 81; E
26.9%; Pred. No. 0.
 -VEMSYEAFDVKNPGDNYKNGAYRYCALSHQDDADDDMTSATDKF 161
 MUTANT STAPHYLOCOCCUS AUREUS V8 PROTEASES
 9:
 20; Mismatches
 001560-264
 DB 4; Length 283,
 67;
 Indels
 30;
 1;
 Gaps
 Gaps
 1;
 7;
```

RESULT 10 US-08-523-373-7

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QY
 RESULT 11
US-08-657-192-3
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 Sequence 3, Apprix No. 5747321
 Matches
 Query Match
 GENERAL INFORMATION:
 TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
 PRIOR APPLICATION UMBER: JP 6-296028
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna N. 607
 APPLICANT: Yabuta, Masayuki APPLICANT: Ohsuye, Kazuhiro TITLE OF INVENTION: PROCESS NUMBER OF SEQUENCES: 24
 COMPUTER
 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION:
 APPLICANT: YABUTA, Masayuki APPLICANT: OHSUYE, Kazuhiro
 MOLECULE TYPE:
 TELECOMMUNICATION INFORMATION: TELEPHONE: 703-836-6620
 PRIOR APPLICATION DATA;
APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP*1994
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: |US/08/523,373
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 ADDRESSEE: BURNS, DOANE,
 289
 123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLF-MIDKWGQ 180
 STREET: 055
CITY: Alexandria
 Match 8.0%; Local Similarity 30.5%;
 STRANDEDNESS:
TOPOLOGY: lir
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 ADDRESSEE: BUKNO, - Street
 COUNTRY:
 STATE:
 CITY: Alexandria
 STREET:
 TYPE: amino acid
 REFERENCE/DOCKET NUMBER:
 FILING DATE:
 COUNTRY:
 ZIP: 22313-1404
 ADDRESSEE:
 REGISTRATION NUMBER:
 CLASSIFICATION:
 ENGTH:
 TGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDRLYRRHHRWGR 347
 7, Application US/08523373
5. 6037145
 INFORMATION:
 22314-3187
READABLE FORM:
TYPE: Floppy disk
 Application US/08657192
 Virginia
 E: BURNS, DOANE, SWECKER & MATHIS P.O. Box 1404
 532 amino acids
 United States
 703-836-2021
 Conservative
 linear
 PatentIn Release #1.0, Version #1.30
 peptide
 05-SEP+1995
 not relevant
 PROTEASES
 PROCESS FOR PRODUCTION OF PROTEIN
 MUTANT STAPHYLOCOCCUS AUREUS V8
 36,607
 15; Mismatches
 Score 80.5; DB 3; Pred. No. 2.2;
 001560-251
 SWECKER & MATHIS
 25;
 Length 532;
 Indels
 Gaps
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 US-08-523-373-5
 RESULT 12
 sequence 5, Application US/08523373 Patent No. 6037145
 Matches
 Query Match
 GENERAL
 TELEFAX: (703) 836-20 INFORMATION FOR SEQ ID NO:
 FILING DATE: 07-SEP-1994
PRIOR APPLICATION UNMBER: JP 6-2
APPLICATION UNMBER: JP 6-2
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
 SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/523,373
 SEQUENCE CHARACTERISTICS:
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
TELECOMMUNICATION INFORMATION:
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
 CORRESPONDENCE ADDRESS
 NUMBER OF SEQUENCES:
 APPLICANT:
 MOLECULE TYPE: protein
 FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
 289 TGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDIHFAND 342
 123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFMID 176
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 COUNTRY: USA
ZIP: 22314-3187
 REFERENCE/DOCKET NUMBER:
 NAME:
 APPLICATION NUMBER: JP 6 FILING DATE: 07-SEP-1994
 FILING DATE:
 STATE:
 STREET:
 TOPOLOGY: li
 TELEPHONE:
 APPLICATION NUMBER:
 FILING DATE:
 APPLICATION NUMBER:
 OPERATING SYSTEM:
 REGISTRATION NUMBER:
 ADDRESSEE:
 Local Similarity 31.5 es 17; Conservative
 LENGTH:
 INFORMATION:
 Alexandria
: VA
 amino acid
 Meuth,
 344 amino acids
 E: BURNS, DOANE, 9
 Ohsuye, Kazuhiro
 Yabuta, Masayuki
 linear
 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
 05-SEP-1995
 703)
 03-JUN-1996
 Donna M.
 Donna M.
 single
 836-2021
 8.0%;
 836-6620
 PROCESS
 JP 7-170086
 Release #1.0, Version #1.30
 JP 6-296028
 JP 6-238595
 US/08/657,192
 36,607
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 13;
 001560-251
 SWECKER & MATHIS
 001560-264
 Score 80; Pred. No.
 FOR PRODUCTION OF PROTEIN
 DB 1; Length 344;
 24;
 Indels
 0;
 Gaps
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 RESULT 13
US-08-523-373-6
 В
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 ; TYPE: amino acid
; STRANDENNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-523-373-5
 ; MOLECULE TYPE: US-08-523-373-6
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Best Local Similarity
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COMPUTER FEADABLE FORM:
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MEDIUM
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LENGTH: 344 amino acids
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 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 TELECOMMUNICATION INFORMATION: TELEPHONE: 703-836-6620 TELEFAX: 703-836-2021
 APPLICATION NUMBER: JP 6-296028 FILING DATE: 07-NOV-1994 ATTORNEY/AGENT INFORMATION:
 APPLICATION NUMBER: JP 6-238595 FILING DATE: 07-SEP-1994 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA:
 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
 APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS
 123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFMID 176
 123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFMID 176
289 TGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDIHFAND 342
 TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
 289 TGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDIHFAND 342
 NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
 CLASSIFICATION:
 APPLICATION NUMBER: US/08/523,373 FILING DATE: 05-SEP-1995
 STREET: 699 Prince CITY: Alexandria
 Match 8.0%;
Local Similarity 31.5%;
 ADDRESSEE:
 17;
 ٧A
 699 Prince Street
 Conservative
 Conservative
 BURNS, DOANE, SWECKER & MATHIS
 peptide
 8.0%;
 PROCESS FOR PRODUCTION OF PROTEIN
 36,607
 13; Mismatches
 Score 80; DB 3; Length 392; Pred. No. 1.6; 13; Mismatches 24; Indels
 Score 80; DB 3; Length 344; Pred. No. 1.3;
 001560-251
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 0;
 Gaps
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 0
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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-523-373-24
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US-08-523-373-22
 RESULT 14
US-08-523-373-24
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Best Local Similarity 31.4
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 Patent No. 6037145
GENERAL INFORMATION:
 Sequence 22, Application US/08523373 Patent No. 6037145 GENERAL INFORMATION:
 TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO: 24:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001560-2
 APPLICATION NUMBER: US/08/523,373
FILING DATE: 05-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
 ZIP: 2017 COMPUTER READABLE FORM:
TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DC
 APPLICANT: Yabuta, Masayuki APPLICANT: Ohsuye, Kazuhiro TITLE OF INVENTION: PROCESS
 NUMBER OF SEQUENCES:
 SEQUENCE CHARACTERISTICS:
 TELECOMMUNICATION INFORMATION:
 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
 APPLICANT: Yabuta, Masayuki APPLICANT: Ohsuye, Kazuhiro
 TITLE OF INVENTION:
 165 TGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDIHF 215
 123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLF 173
 LENGTH:
 CITY: Alexandria STATE: VA
 LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: not relev.
 TELEPHONE: 703-836-2021
COUNTRY: USA
ZIP: 22314-3187
 STREET:
 COMPUTER:
 CITY: Alexandria
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 ADDRESSEE:
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 Application US/08523373
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 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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 703-836-6620
 not relevant
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COMPUTER READABLE FORM;

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
CORRENT ASSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,373
FILING DATE: 05-SEP-1995
FILING DATE: 07-SEP-1994
PRIOR APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-NOV-1994
ATTORNEY/ACENT INFORMATION:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/ACENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36.607
REFERENCE/DOCKET NUMBER: 30.1580-251
TELECOMMUNICATION NUMBER: 3703-836-2021
INFORMATION FOR SEQ ID NO: 22:
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
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OM protein - protein search, using sw model

Run on: December 20, 2002, 15:49:10 ; Search time 45 Seconds (without alignments)

408.037 Million cell updates/sec

Title: Perfect score: 1003 1 SKSVIAAARAIQADAMANAY......LFMIDKWGQCPRLIQELKLI 191

US-10-008-355-2\_COPY\_522\_712

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs; 96134422 residues

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| 29                 | 28                 | 27                | 26                 | 25                 | 24                 | 23     | 22                 | 21                | 20                 | 19     | 18                 | 17                | 16     | 15     | 14     | 13                 | 12     | 11     | 10                 | ø        | 8                  | 7                  | o                  | ر.<br>د            | 4                  | ω      | ٨      | _            | Result<br>No.  |
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| 79.5               | 79.5               | 79.5              | 80                 | 80                 | 80                 | 80     | 80                 | 80.5              | 80.5               | 81     | 81                 | 81                | 81.5   | 81.5   | 82     | 82.5               | 83     | 84     | 84                 | 86       | 86.5               | 89.5               | 89.5               | 89.5               | 90                 | 93     | 95     | 334          | Score          |
| 7.9                |                    |                   | ٠                  | 8.0                |                    |        |                    |                   |                    |        |                    | ٠                 | ٠      |        | ٠      |                    |        |        | 8.4                | . 8.6    | 8.6                | 8.9                | 8.9                | 8.9                | 9.0                | 9.3    | 9.5    | 33.3         | Query<br>Match |
| 747                | 389                | 240               | 3433               | 2043               | 357                | 342    | 336                | 434               | 325                | 1104   | 663                | 239               | 603    | 493    | 402    | 759                | 869    | 968    | 729                | 1060     | 576                | 3411               | 3411               | 856                | 711                | 513    | 507    | 716          | Length         |
| N                  | N                  | N                 | μ.                 | N                  | N                  | N      | <u> </u>           | N                 | N                  | N      | N                  | N                 | N      | N      | 2      | N                  | N      | N      | N                  | N        | N                  | ۳                  | -ب                 | N                  | N                  | N      | N      | N            | DB             |
| н82943             | н86656             | C89967            | GNWVKV             | T18524             | S21758             | G89873 | PRSASK             | A29525            | E75404             | A60999 | AG0782             | в89967            | T04733 | G90604 | C87291 | AE1686             | D81832 | S46992 | AF3591             | н86686   | в39228             | GNWVYP             | GNWVY              | T13159             | S70660             | D96980 | T34152 | G82627       | ID             |
| hypothetical prote | hypothetical prote | serine proteinase | genome polyprotein | scavenger receptor | glutamic acid-spec |        | glutāmyl endopepti | methyl coenzyme M | ABC transporter, A | 4      | colicin I receptor | serine proteinase | ct     |        | н.     | pyruvate formate-1 | bir    | o      | alkaline phosphata | <u>с</u> | flagellin B - Camp | genome polyprotein | genome polyprotein | E1B-55kDa-associat | transferrin-bindin | ຜ      | al     | thetical pro | Description    |

| 45     | 44     | <b>4</b> 3          | 42                 | 41                 | 40                 | 39                 | 38                 | 37                 | 36                 | 35                 | 34                   | 33                 | 32                 | 31                 | 30                 |
|--------|--------|---------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------------------|--------------------|--------------------|--------------------|--------------------|
| 77     | 77     | 77                  | 77                 | 77.5               | 77.5               | 77.5               | 77.5               | 78                 | 78                 | 78                 | 78                   | 78.5               | 78.5               | 78.5               | 78.5               |
| 7.7    | 7.7    | 7.7                 | 7.7                | 7.7                | 7.7                | 7.7                | 7.7                | 7.8                | 7.8                | 7.8                | 7.8                  | 7.8                | 7.8                | 7.8                | 7.8                |
| 412    | 332    | 170                 | 161                | 3391               | 647                | 647                | 515                | 3432               | 1084               | 846                | 271                  | 3388               | 803                | 498                | 289                |
| 2      | N      | ν                   | N                  | -                  | μ                  | ب                  | ν                  | ۳                  | N                  | ν                  | N                    | ш                  | 2                  | N                  | 2                  |
| H75484 | C95077 | AD1934              | H84458             | GNWV26             | G91277             | G86118             | A70905             | GNWVJE             | C82931             | T04533             | G83780               | GNWVDP             | T34994             | н81782             | A89824             |
|        |        | hypothetical, prote | hypothetical prote | genome polyprotein | 2',3'-cyclic-nucle | 2',3'-cyclic-nucle | hypothetical prote | genome polyprotein | hypothetical prote | hypothetical prote | . hypothetical prote | genome polyprotein | probable long-chai | adhesin MafB2 NMA2 | conserved hypothet |

## ALIGNMENTS

hypothetical protein XF1887 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000 C;Accession: G82627

R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82315; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 below A;Accession: G82627

A; Status: preliminary

A; Molecule type: DNA A; Residues: 1-716 <SIM>

A;Cross-references: GB:AE004008; GB:AE003849; NID:g9106961; PIDN:AAF84693.1; GSPDB:GN A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajina, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.R.G.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L., A.Reference number: A59328

A;Contents: annotation C;Genetics: A;Gene: XF1887

Query Match Local Similarity 40.074; Conservative 33.3%; 40; Score 334; DB 2; Pred. No. 2.1e-22; 0; Mismatches 53; Length 716; Indels 18;

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| Db                                                                   | Qy                                                                   | DЬ                                                                   | Qy                                                                | Db                                                     | Qy                                                                |
|----------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|-------------------------------------------------------------------|--------------------------------------------------------|-------------------------------------------------------------------|
| 650                                                                  | 126                                                                  | 591                                                                  | 68                                                                | 546                                                    | 8                                                                 |
| 650 NSGSPVLDAHGKLVGLAFDGNWESVSSNWVFDPVMTRTIAVDSRVVQWIMTEVAPAPHLL 709 | 126 NSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFMIDKWGQCPRLI 185 | 591 YTPFTTLQGVMAK-NTGVEPFDSPKSLINAIKAKSYANLADQRIGTVPVNFLSDLDITGG 649 | 68 YNYHTTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGG 125 | 546 ARPIYLQALAD-YNKSHGKFYYPDANSSLRITFGHYKGYSPKDGVE 590 | 8 ARAIQADAMANAYAIEKGKRLFFAGLREMYPGRALPSDANFTMRMSYGSIKGYEPQDGAW 67 |
|                                                                      |                                                                      |                                                                      |                                                                   |                                                        |                                                                   |

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186 QELKL 190 :|| |

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 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bact.
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: D96980
 sensory transduction histidine kinase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: D96980
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D96980
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A:Introns: 62/2; 109/2; 144/3; 182/2; 208/3; 252/3; 324/3; 370/3
C:Superfamily: Caenorhabditis elegans hypothetical protein F07GI1.3
 R;Bradshaw, H.; Stellyes, L.
submitted to the EMBL Data Library, November 1995
submitted to the EMBL Data Control of C. elegans cosmid
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 A;Cross-references: GB:AE001437; PIDN:AAK78631.1; PID:915023529; GSPDB:GN00168 A;Experimental source: Clostridium acetobutylicum ATCC824
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 A;Cross-references: EMBL:U41007; PIDN:AAA82261.1; CESP:C33H5.2 A;Experimental source: strain Bristol N2
 A; Reference number: A; Accession: T34152
 C;Accession: T34
R;Bradshaw, H.;
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 A; Molecule type: DNA
A; Residues: 1-513 < KUR>
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 26-May-2000
 hypothetical protein C33H5.2 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
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 A; Cross-references:
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Best Local
 Matches
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 379
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 Local Similarity es 37; Conserv
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 RTKNYGRYAENGQLHIAFLSNNDITGGNSGSPVFDKNGRLIGL--AFDGNWEAMSGDI-- 154
 KELNL
 FVYEKKGGVIDVYKTEKGRYQNKYTQNYLETIFNNGKVIISTILP--DDYS-EDNLSKCY 152
 FTMRMSYGSIKGYEPQDGAWYNYHT-----TGKGVLEKQDPKSDEFAVQENILDLF 98
 SGSPVFDKNGRLIGLAFDGNWEA---MSGDI-EFEPDLQR 162
 PQNANYTWLHYPPVLVNGLEKYEVEENVITHLKTINW-----
 KQDPK------SDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGN 126
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 T34
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 DB 2;
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 56;
 45; Indels
 Length 507;
 Length 513;
 Indels
 ----VEDEVKTG- 378
 28;
 50;
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 A;Gene: tbp2
 C; Genetics:
 C; Accession:
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 Query Match
Best Local S
Matches 42
 Genetics:
 Matches
 Query Match
 607
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 566
 518
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 62
 72
 Local
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R;Gabler, S.; Schuett, H.; Groitl, P.; Wolf, H.; Shenk, J. Virol. 72, 7960-7971, 1998
A;Title: EIB-55kilodalton-associated protein: A cellular A;Reference number: 217615; MUID:98406198; PMID:9733834
A;Accession: T13159
 C:Species: Homo sapiens (man)
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C:Accession: T13159
 Mol. Microbiol. 19, 159-169, 1996
A; Title: Molecular characterization of hybrid Tbp2 proteins from Neisseria meningitid A; Reference number: S70659; MUID:96419172; PMID:8821945
 A;Cross-references: EMBL:AJ007509; NID:g3319955; PIDN:CAA07548.1; PID:g3319956
A;Experimental source: HeLa cell line
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 C; Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent recepto
 A; Note: the nucleotide sequence was
 A; Molecule type: DNA
A; Residues: 1-711 <L
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 C;Species: Neisseria meningitidis
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
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 δÃ
 A;Cross-references: EMBL:Z50731; NID:g1177568; PIDN:CAA90598.1; PID:g1177569
 R; Legrain, M.; Findeli, A.; Villeval, D.; Quentin-Millet, M.J.;
 249 SYGVRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQLGEEPFS----YGYG 305
 155
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les 42; Conser
 19 AYAIEKGKRLFFAGLREMYPGRALPSDA--NFTMRM-----SYGSIKGYEPQDGAWYNYH 71
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TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYG-RYAENGQLHIAFLSNNDITG-----
 SUNDITGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYV 171
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 9.0%;
 8.9%; Score 89.5; D
25.1%; Pred. No. 5.2;
tive 22; Mismatches
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 239
 DB 2;
 ç
 DB
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 56;
 2;
 66;
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 NEGEKKITGTL----
 Indels
 protein with RNA-binding act
 Data
 Dobner,
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 Jacobs,
 47;
 42;
 <MAT:
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 909
 August
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N:Contains: capsid protein C; envelope protein M; major envelope protein E; protein NS4a; nonstructural protein NS4b; nonstructural protein NS5 C; Species: yellow fever virus C; Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 19-Jan-2001 C; Accession: S07757 R; Dupuy, A.; Despres, P.; Cahour, A.; Girard, M.; Boulov Mucleic Acids Res. 17, 3989 1000
 GNWVYP
 F:286-778/Product: major envelope protein E #status predicted <MEE>
F:740-753/Domain: transmembrane #status predicted <TM3>
F:755-778/Domain: transmembrane #status predicted <TM3>
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F:779-1187/Product: nonstructural protein NS1 #status predicted <NS1>
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F:1159-134/Product: nonstructural protein NS2a #status predicted <N2A>
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F:1355-1484/Product: nonstructural protein NS2b #status predicted <N2B>
F:1465-2107/Product: nonstructural protein NS3 #status predicted <NS3>
F:1682-169/Region: nucleotide-binding motif A (P-loop)
F:1773-1776/Region: DEAH motif
 F;211-285/Product: envelope protein M *status predicted <EPM>
F;249-269/Domain: transmembrane *status predicted <TM1>
F;271-285/Domain: transmembrane *status predicted <TM2>
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 F;2108-2394/Product: nonstructural protein NS4a #status predicted <N4A>F;2395-2506/Product: nonstructural protein NS4b #status predicted <N4B>F;2507-3411/Product: nonstructural protein NS5 #status predicted <NS5>F;2507-3411/Product: nonstructural protein NS5 #status predicted <NS5>F;134,150,172,266,594,755,908,986,1796,2062,2320,2346,2408,2467,2720,2734,2740/Binding
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 C;Species: yellow fever virus
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 19-Jan-2001
 망
 Вb
 B
 A; Reference number: A03914; MUID:85272570; A; Accession: A03914
 A;Tille: Nuclectide sequence of yellow fever virus: implications A;Reference number: A03914; MUID:85272570; PMID:4023707
 R; Rice, C.M.; Lenches, E.M.; Eddy, S.R.; Science 229, 726-733, 1985
 C; Accession: A03914
 genome polyprotein
 A;Cross_references: GB;X03700; GB:K02749; NID:g59338; PIDN:CAA27332.1; PID:g59339
 A; Residues: 1-3411 <RIC>
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 1542
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 1586 AVPGKNVVNVQTKPS-
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 19 AYAIEKGKRLFFAGLREMYPGRALPSDANFTMRM-SYGSIKGYEPQDGAWYNYH-----
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 -TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSP 130
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 capsid protein C;
 Similarity
 nonstructural protein NS4b;
low fever virus
 genomic RNA
 Conservative

 yellow fever virus (strain 17D)

 8.9%;
25.5%;
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 envelope protein M; major envelope
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 Score 89.5;
Pred. No. 31
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 Mismatches
 Shin,
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 1655
 DB 1;
 S.J.;
 46;
 Length 3411;
 Sheets, R.L.; Strauss, J.H.
 Indels
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 NDVIGCFADFE
 47;
 nonstructural protein;
 protein E; nonstructurants
 for flavivirus gene exp
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 E; nonstructur
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Дb

232

AWYNYTTGKOYLEKODPKSDEFAVOENILDLFRTKNYGRYAENGOLHIAFISNDITGG 125

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F;1134/Product: nonstructural protein NS2a *status predicted <N2A>
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F;1485-2107/Product: nonstructural protein NS2b *status predicted <N2B>
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C;Species: Campylobacter jejuni
C;Date: 20-Sep-1991 #sequence_revision 20-Sep-1991 #text_change 26-Aug-1999
 J. Biol. Chem. 265, 17798-17804, 1990
A;Title: Structural and functional analysis of two Campylobacter jejuni flagellin gen A;Reference number: A39228; MUID:91009243; PMID:2211662
A;Accession: B39228
 C;Accession: B39228
R;Nuijten, P.J.M.; van Asten, F.J.A.M.; Gaastra,
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 F;2108-2394/Product: nonstructural protein NS4a #status predicted <N4A>F;2395-2506/Product: nonstructural protein NS4b #status predicted <N4A>F;2395-2507-3411/Product: nonstructural protein NS5 #status predicted <NS5-F;134,150,172,594,908,986,1796,2062,2320,2346,2408,2467,2720,2734,2740/Binding
 A;Cross-references: EMBL:X15062; NID:g62289; IA;Note: the nucleotide sequence was submitted
 A; Title: Nucleotide sequence comparison of the genome of two 17D-204 A; Reference number: S07757; MUID:89282413; PMID:2734112 A; Accession: S07757
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A; Residues: 1-576 < NUI>
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Best Local Similarity
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 Similarity
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31.5%;
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Pred. No. 31;
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Mismatches
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 163
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 .9
 to the EMBL Data Library, April
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 DВ
 46;
 W.; van
 39;
 glycoprotein; nonstructural protei
 Length 3411;
 Indels
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 -DYPSGTSGSP
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 <N2A>
Gaps
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Accession: AF3591
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 A;Gene: dnaE
C;Superfamily: DNA-directed DNA polymerase III alpha
C;Keywords: nucleotidyltransferase
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 A; Molecule type: DNA
A; Residues: 1-729 <KUR>
A; Cross-references: GB: AEC08918; PIDN: AAL53897.1;
 alkaline phosphatase (EC 3.1.3.1) [imported] - Brucella melitensis (strain C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
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 A; MoLecule type: DNA
A; Residues: 1-1060 <STO>
A; Cross-references: GB.AE005176; PID:g12723378;
A; Experimental source: strain IL1403
 Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: H86686
 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, Genome Res. 11, 731-753, 2001
 DNA-directed DNA polymerase (EC 2.7.7.7) [imported] - Lactococcus lactis subsp. N;Alternate names: DNA polymerase III, alpha chain 2 C;Species: Lactococcus lactis subsp. lactis
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 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-200
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 288
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les 45; Conservative
 YHTTGKGVLEKQDPKSDEFAVQENILDL-----FRTKNYGRYAENGQLHIAFLS--NN 120
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 -QLVKNRRMTILVEINYIRTHRTKTGQ 931
 DIFMASSGGGFAYHEAEDYSETEKYDFEKN--LLGIGVTPHPLQNLARRFEGNFTPLA--
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 DALENGFEIEK------PSINLMKIGDFVKNKKIRLGLAHVQGISRDLAKWIV 789
 NSGSPVFDKNGRLIGLAFDGNWEAMSGDI
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 8.4%;
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 Length 729;
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 GSPDB:GN00146
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C;Superfamily:
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 D81832
 RESULT 12
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A;Residues: 1-698 <PAR>
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 A; Title: A novel signaling molecule, p130, A; Reference number: S46992; MUID:94349922; A; Accession: S46992
 A; Experimental source:
 A;Reference number: A81775;
A;Accession: D81832
 R;Parkhill, J.; Achtman, M.; James, Holfoyd, S.; Jagels, K.; Leather, Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a
 C; Superfamily: SH3 homology
F; 104-154/Domain: SH3 homology <SH3>
 A; Molecule type: mRNA
A; Residues: 1-968 <SAK>
 R;Sakai, R.; Iwamatsu, A.; Hirano, N.; Ogawa, EMBO J. 13, 3748-3756, 1994
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 pathogen transferrin-binding protein; tonB-dependent recepto
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83;
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19;
 s.;
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 --HIAFLSUNDITGGNSGSPV 131
 64;
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 S.D.; Churcher, C.; Mungall, K.; Quail,
 Neisseria meningitidis (strain
 Length 968,
 Indels
 H
 Neisseria menigitidis Z2491
 698;
 Mano, H.; Yazaki, Y.; H
 44;
 Gaps
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Rajandre
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 9;
 Z24
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Score

DB

2;

Length

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A; Authors: Kreft; J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoles, N.; Tierrez, A.; Vazquez-Boland, J.A.; A; Title: Comparative genomics of Listeria species.

A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AE1686
A; Status: preliminary
A, Molocula Legislation.
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 R;Nierman, W.C.; Reldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, White, Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
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A;Residues: 1-759 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC97261.1; PID:g16414532; GSPDB:GN00178
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 .; Dominguez-Bernal, G.; D.; Jones, L.M.; Karst, Science 294, 849-852, 20
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.;
 C; Species: Listeria C; Date: 27-Nov-2001
 pyruvate formate-lyase homolog pflA [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
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A;Status: preliminary
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A;Residues: 1-402 <STO>
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 C; Accession: C87291
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37; Conser
 Similarity
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 Conservative
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 Pred. No.
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 Mismatches

 Caulobacter crescentus

 16;
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 71;
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 Length 759;
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 21;
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 Gaps
 Gaps
 Maitournam, A.; Ma
Voss, H.; Wehland,
 593
 552
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 6;
 ; Bloecker
Fsihi, H.
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2002,

17:31:37

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 Вb
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 A; Gene: CC0340
C; Superfamily:
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 Nucleic Acids Res. 29, 2145-2153, 2001
A; Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma A; Reference number: A99512; MUID:21267165; PMID:11353084
 C; Accession: G9(R; Chambaud, I.;
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 A;Cross-references: GB:AE005673; NID:g13421489; PIDN:AAK22327.1; GSPDB:GN00148 C;Genetics:
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378 KYYYSGLLY--YFRNTALSGGSSGSKTVDKNNKIVGIHALGSDLSGLTGSVAFKSE 431
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 254 DG---QDVIYKNHYDIGVAVGTDKGLVVPVVRDADALNLAGIEKTIGDL-----GKRAR 304
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 16;
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 8.2%;
25.0%;
 17;
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Pred. No. 1
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 14;
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 DB
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 ----KAIP-DVN-----AEI 253
 71;
 20;
 2;
 lipoyl/biotin-binding homology
 Samson,
 Length 402
 Length 493;
 Indels
 Indels
 D.;
 46;
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 OM protein - protein search, using sw model
 Database
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Sequence:
 Title:
Perfect score:
 Total number of hits satisfying chosen parameters:
 Searched:
 Scoring table:
 on:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
 Length
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 TBPB_NEIMA
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 112892
 O9ci70 lactococcus
O9sel7 arabidopsis
P54627 drosophila
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 Description
 Q50335 mycoplasma
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3 desulfovibr
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8 mycobacteri
 4 dengue viru
3 d genome po
5 homo sapien
6 j genome po
7 candida alb
1 d genome po
3 strongyloce
5 w genome po
6 drosophila
 ·borrelia bu
escherichia
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ureaplasma
 trypanosoma
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379 127 334

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333 79

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22 IEKGKR--LFFAGLREMYPGRALPSDANFTMRMSYGSIKGYEPQDGAWYNYHTTGKGVLE

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RESULT 2

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|-------------------------------------|----------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|--------------------------------------------------------------------------|-----------------------|------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Be.<br>Ma                           | O K R R R R                                                                      | 388888888888                                                                                                                                                                                                                                                                                                   | 3 6 6 8 5 6 8 8                                                                                                                                          | × 2 2 2 2 2                                                                         |                                                                          | SU<br>42              |            |                                                                                                                                                                             |
| Query Matc<br>Best Local<br>Matches | EMBL; U WORMPep InterPr Pfam; p ProDom; Hypothe SEQUENC                          | AND ZI                                                                                                                                                                                                                                                                                                         | [1] SEQUE STRAI Brads Submi                                                                                                                              | Caenc<br>Caenc<br>Eukar<br>Rhabd<br>NCBI_                                           | 15-JU<br>15-JU<br>15-JU<br>Hypot                                         | LT 1<br>CAEEL<br>YY42 |            | 60000000000000000000000000000000000000                                                                                                                                      |
|                                     | EMBL; U4100 WormPep; C3 InterPro; I Pfam; pF016 ProDom; PD0 Hypothetica SEQUENCE | AND ZK381.  SWISS-PRO Gen the B European B by non-p fied and t ties requi                                                                                                                                                                                                                                      | [1] SEQUENCE FROM STRAIN-Bristol Bradshaw H., S Submitted (DEC -!- SIMILARITY                                                                            | C33H5.2. Caenorhabditis Caenorhabditis Eukaryota; Met Rhabditidae; P NCBI_TaxID=623 | 15-JUL-1998<br>15-JUL-1998<br>15-JUL-1998<br>15-JUL-1998<br>Hypothetical | CAEEL                 |            | 75.5<br>75.5<br>75.5<br>74.5<br>74.5<br>74.5<br>74.5<br>74.5                                                                                                                |
| h<br>Similarity<br>37; Conservat    | 7;<br>3H5<br>PRO<br>PRO<br>97;<br>97;<br>041<br>1 p                              | AND ZK381.2.  This SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinforma the European Bioinformatics Institute. The by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch). | SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-Bristol N2; Bradshaw H., Stellyes L Submitted (DEC-1995) to -!- SIMILARITY: BELONGS -!- SIMILARITY: BELONGS | ശരയ                                                                                 | 8 (Rel.<br>8 (Rel.<br>8 (Rel.<br>al 58.6                                 | S                     |            | 77777777777777777777777777777777777777                                                                                                                                      |
| 9.<br>Y 23.<br>rvative              | 82261.1<br>CE0414<br>75; DUF<br>F23; 1.<br>DUF23;<br>ein.<br>; 5857              | Nor entry is cop<br>Swiss Institute<br>Bioinformatics<br>Profit institut<br>this statement<br>ires a license<br>ail to license                                                                                                                                                                                 | 1 2 20                                                                                                                                                   | elegans.<br>Izoa; Nema<br>loderinae                                                 | 36,<br>36,<br>36,                                                        | TANDARD;              |            | 3391<br>33391<br>3432<br>3432<br>784<br>814<br>1254<br>1254<br>1255<br>1255<br>793                                                                                          |
| 19 %                                | L;<br>16.<br>723.<br>11.                                                         | copyr<br>itute o<br>tics In<br>stituti<br>nent is<br>ense ag                                                                                                                                                                                                                                                   | the I                                                                                                                                                    | ns.<br>Nematoda;<br>inae; Cae                                                       | Created<br>Last sec<br>Last and<br>protein                               |                       |            | 44444444444                                                                                                                                                                 |
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| 95;<br>No.<br>smatc                 | AFB047FA:                                                                        | yright. It is prod of Bioinformatics Institute. There as long as is not removed. Unagreement (See htt. isb-sib.ch).                                                                                                                                                                                            | EMBL/GenBank/DDBJ databas                                                                                                                                | madore<br>bditis                                                                    | e upda<br>ion up                                                         | 507                   | ALIGNMENTS | a_DEN26<br>a_JAEV2<br>a_JAEV5<br>a_JAEV5<br>a_JECOLI<br>a_EEVVB<br>a_EEVVE<br>a_EEVVE<br>a_EEVVE<br>a_EEVVP<br>a_EEVVP                                                      |
| 1;<br>1;                            | C1886                                                                            | 00 - 100                                                                                                                                                                                                                                                                                                       | C/DDBJ                                                                                                                                                   | ٠.                                                                                  | ite)<br>odate)<br>i chro                                                 | AA.                   | เช         |                                                                                                                                                                             |
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DE POCTEINS
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OS Yellow feve
OC Viruses; ss
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RT FINITUS-85; SS
OC PLAVIUS-85;
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 InterPro; IPRO01410; DEAD.
InterPro; IPRO01410; DEAD.
InterPro; IPRO0159; Flavi_NS1.
InterPro; IPRO0157; Flavi_NS2A.
InterPro; IPRO00752; Flavi_NS2B.
InterPro; IPRO00404; Flavi_NS2B.
InterPro; IPRO01528; Flavi_NS4B.
InterPro; IPRO01528; Flavi_NS4B.
InterPro; IPRO01122; Flavi_NS5.
InterPro; IPRO01122; Flavi_OppsidC.
InterPro; IPRO00385; Flavi_DycoprotE.
InterPro; IPRO00385; Flavi_Dicase.
InterPro; IPRO02877; FtsJ.
InterPro; IPRO02877; FtsJ.
InterPro; IPRO01650; Helicase_C.
InterPro; IPRO01650; Helicase_C.
 P03314; 042028;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: Capsid protein C (Core protein); Matrix protein (Envelope protein M); Major envelope protein E; Nonstructural proteins NS1, NS2A, NS2B, NS4A and NS4B; Protease/helicase
(EC 3.4.21.98) (NS3); RNA-directed RNA polymerase (EC 2.7.7.48)
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 EMBL; X03700; CAA27332.1;
 ### MEDLINE=85272570; PubMed=4023707; MEDLINE=85272570; PubMed=4023707; MEDLINE=85272570; PubMed=4023707; Shin S.J.,
 Viruses; ssRNA
Flavivirus,
 Nucleotide sequence of yellow
 ellow fever virus (strain 17D).
Tiruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EW European Bioinformatics Institute. There are no restrictions of the company of the contract of t
 precursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'. CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate (RNA)(N).
 FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B AR HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCT NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
 SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS
 CATALYTIC
 PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID PROTEIN C AND MRNA.
 A03914
 PF00271;
PF00869;
PF00948;
PF00949;
PF00972;
PF01002;
PF01003;
PF01004;
 P14336; 1S
S; S07.001;
 rus gene expression and 229:726-733(1985).
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; Flavi_glyCoprot; 1.
; Flavi_NS1; 1.
; Flavi_NS5; 1.
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; Flavi_NS4B; 1.
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 ; helicase_C; 1
 ACTIVITY: Hydrolysis of four peptide bonds in the viral polyprotein, commonly with Asp or Glu in the P6 Cys or Thr in P1 and Ser or Ala in P1'.
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 STANDARD;
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 NS2B, NS4A AND NS4B ARE MEMBRANE-RELATED FUNCTION.
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AC p19901;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Genome polyprotein [Contains: Capsid protein C (Core protein); Matrix
DE protein (Envelope protein M); Major envelope protein E; Nonstructural
DE proteins NS1, NS2A, NS2B, NS4A and NS4B; Protease/helicase
(EC 3.4.21.98) (NS3); RNA-directed RNA polymerase (EC 2.7.7.48)
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 pfam; PF01570; Flavi_propep; 1.
pfam; PF01728; Fts5; 1.
pfam; PF021823; Ftavi_glycop_C; 1.
proDom; PD001496; Flavi_NS1; 1.
ProDom; PD001556; Flavi_glycoprotE; 1.
prodom; PD001556; Flavi_glycoprotE; 1.
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 Core protein; ATP-binding;
 SMART; SM00490; HELICC; 1. Polyprotein; Glycoprotein; Transferase; RNA-directed RNA
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 Score 89.5;
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NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
PROTEASE/HELICASE (NS3).
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NONSTRUCTURAL PROTEIN NS4B.
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 Mismatches
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 pfam; pr00869; Flavi_giycoprot; 1.
pfam; pr00948; Flavi_NS1; 1.
pfam; pr00949; Flavi_NS5; 1.
pfam; pr00949; Flavi_NS5; 1.
pfam; pr00972; Flavi_NS2B; 1.
pfam; pr01002; Flavi_NS2B; 1.
pfam; pr01003; Flavi_NS2B; 1.
pfam; pr01004; Flavi_NS2B; 1.
pfam; pr01005; Flavi_NS4B; 1.
pfam; pr01349; Flavi_NS4B; 1.
pfam; pr01349; Flavi_NS4B; 1.
pfam; pr01350; Flavi_NS4B; 1.
pfam; pr01350; Flavi_NS4B; 1.
pfam; pr01570; Flavi_NS4B; 1.
pfam; pr01570; Flavi_NS4B; 1.
pfam; pr015832; Flavi_Stopep; 1.
pfam; pr01728; FtsJ; 1
pfam; pr001496; Flavi_Stopenct; 1.
proDom; p0001556; Flavi_StopenctE; 1
smarr; sm00490; HELICC; 1.
 InterPro; IPR001410; DEAD.

InterPro; IPR00069; Flavi_M.

InterPro; IPR001157; Flavi_NS1.

InterPro; IPR000752; Flavi_NS2B.

InterPro; IPR000407; Flavi_NS2B.

InterPro; IPR000404; Flavi_NS4B.

InterPro; IPR001528; Flavi_NS4B.

InterPro; IPR000208; Flavi_NS5.

InterPro; IPR0001122; Flavi_GapsidC.

InterPro; IPR000336; Flavi_Glycorro;

InterPro; IPR000336; Flavi_Glycorro;
 InterPro;
Pfam; PF0(
 Nucleic Acids Res. 17:3989-3989(1989).

- PUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE PUNCTION: THE SMALL PROTEING A POSSIBLE MEMBRANE-RELATED FUNCTION.

- POSSIBLE MEMBRANE-RELATED FUNCTION.

- CATALYTIC ACTIVITY; Hydrolysis of four peptide bonds in the viprecursor polyprotéin, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'.

- CATALYTIC ACTIVITY; N nucleoside triphosphate = N diphosphate
 MEDLINE-89282413; PubMéd-2734112;
Dupuy A., Despres P., Cahour A., Girard M.,
"Nucleotide sequence comparison of the genor
 Polyprotein; Glycoprotein; Toore protein; Coat protein;
 HSSP;
 PIR; S07757; GNWVYP.
 EMBL;
 or send
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 between
 fever vaccines.
 SEQUENCE FROM N.A. MEDLINE-89282413;
 NCBI_TaxID=11091;
 Flavivirus.
 Viruses; ssRNA
 (NS5)].
Yellow fever
 InterPro;
 InterPro;
 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EMEuropean Bioinformatics Institute. There are no restriby non-profit institutions as long as its content
 (RNA)(N).:
SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS
 X15062; CAB37419,1;
 P14336;
 an email to license@isb-sib.ch).
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 IPR001850;
IPR002535;
 IPR001650;
 M'AND GLYCÓPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF C AND MRNA;
 virus
 ; Coat protein; Envelope protein; Hydrolase; Transmembrane; Nonstructural protein.

1 1 REMOVED FROM CAPSID PROTEIN
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 irus (strain Pasteur 17D-204).
positivė-strand viruses, no DNA stage; Flaviviridae;
 helicasė_C;
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 Flavi_capsidC.
Flavi_glycoprotE.
Flavi_helicase.
 Flavi_propep
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 NP_BIND
 "Structural and functional analysis of two Camp flagellin genes.";
J. Biol. Chem. 265:17798-17804(1990).
-i- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN
 MEDLINE=91009243;
Nuijten P.J., van
 SEQUENCE FROM N.A.
 NCBI_TaxID=197;
 Campylobacter.
 Campylobacter jejuni
Bacteria; Proteobacteria;
 Flagellin
 CARBOHYD
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 19
FORM THE FILAMENTS OF BACTERIAL FLAGELLA
 IVNRNGEVIGLYGNG---ILVGDNSFVSAISQT 1655
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 AFLVRNGKKL:
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NONSTRUCTURAL PROTEIN US.2A.
NONSTRUCTURAL PROTEIN US.2A.
NONSTRUCTURAL PROTEIN US.2B.
PROTEASE, HELICASE (NS.3).
NONSTRUCTURAL PROTEIN US.4A.
NONSTRUCTURAL PROTEIN US.4B.
NONSTRUCTURAL PROTEIN US.4B.
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BY SIMILARITY.
 Score 89.5;
Pred. No. 1
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 CAPSID PROTEIN
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PIR; B39228; B39228
InterPro; IPR001492; Flagellin.C.
InterPro; IPR001029; Flagellin_C.
Pfam; PF00700; Flagellin_C; 1.
Pfam; PF00700; Flagellin_C; 1.
PRINTS; PR00207; FLAGELLIN.
 MEDLINE-21235186; PubMed-11337471;
Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
Genome Res. 11:731-753(2001).
-i- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).
-i- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 DP3A_LACLA
Q9CI70;
 15-JUN-2002 (Rel. 41, Last sequence update)
DNA polymerase III alpha subunit (EC 2.7.7 2
DNAE OR LL0496.
 Flagella.
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 Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 or send an email to license@isb-sib.ch).
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 66 AWYNYHTTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGG 125
 AND CHI) AND WITH THE BETA CHAIN (BY SIMILARITY) SUBCELULAR LOCATION: Cytoplasmic (By similarity: SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-C SUBFAMILY.
 SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THE CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CO DIMERIZATION TO FORM THE POLITI' COMPLEX. POLITI' ASSOCIATES THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', F
 SUBUNIT: HETEROPOLYMER OF FLAA AND FLAB.
SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
 + (DNA)(N).
 QASK----DENGKLYLTSADGRGIKITGDI
 NSGSPVFDKNGRLIGLAFDGNWEAMSGDI
 ATYDVKTTGVYAI-KEGTTSQDFAINGVVIGQI---NYKDGDNNGQLVSAINAVKDTTGV 286
 PD000316; Flagellin_C; 1.
 575
 Conservative
 0
 AA;
 STANDARD;
 entry
 59728 MW;
 8.6%;
 0
 S
 copyright.
 15;
 Score 86.5; D
Pred. No. 2.2;
 BY SIMILARITY
 PRT;
 D0531AF308A7BF1D CRC64;
 Mismatches
 1060
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 n update)
2.7.7.7).
 (By similarity).
(By similarity).
 25
 AA
 DB 1;
produced
 39;
 Length 575;
 Indels
through a collaboration
 restrictions
 and
 DELTA', PSI
 EMBL outstation
 AND THETA
 for commercial
 collaboration
 CORE
 Gaps
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HHOA_ ARATH
AC OPSELT
DT 16-OCT
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OC Eukary
OC Sperma
OC EUKARY
IN INTERPORT
RN [1]
RP SEQUEN
RA LENSCH
RT A LONG
RL SUBMIT
RN [2]
RP SEQUEN
RA HARTIS
RA MAYER
RA HARTIS
RA WEICHS
RA Kreis
RA Kreis
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 RESULT
 Matches
 Query Match
STRAIN-cv. Columbia;

MEDLINE-20083488; PubMed=10617198;

Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,

Pohl T., Duesterhoeft A., Stiekema W., Entlan K.-D., Terryn N.,

Harris B., Ansorge W., Brandt P., Grivell L., Rieger M.,

Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,

Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,

Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,

Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,

Kreis M., Delseny M., Puigdomenech P., Watson M., Boutry M., Bancroft I.,

Kreis M., Delseny M., Bilham L., Robben J.,

Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,

Vos P., Hoheisel J., Bilham L., Robben J.,

McGulladh B., Bilham L., Robben J.,

Vandenbussche F.,
 OSSEL7: 049507;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protease HhoA, Chloroplast precursor (EC 3.4.21.-).
HHOA OR ATAG18370 OR F28J12.30.
Arabidopsis thaliana (Mouse-ear cress).
 a homolog
 use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb
 Submitted
 SEQUENCE FROM N.A. Lensch M.H.A., Sokolenko A., Herrmann
 Eukaryota; Viridiplantae; Streptophyta; Embryo Spermatophyta; Magnoliophyta; eudicotyledons;
 Pfam; PF01336; tRNA_anti; 1. Pfam; PF02231; PHP_N; 1. SMART; SM00481; POLITIAC; 1.
 SEQUENCE FROM N.A
 Lensch M.H.A., Sokolenko A., Herrmann R.G.;
"Identification and characterization of the chloroplast
a homolog to the bacterial periplasmic protease HhoA.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
 HHOA_ARATH
 InterPro; IPR004805; InterPro; IPR004365;
 EMBL; AE006285; AAK04594.1; -.
 or send an email to license@isb-sib.ch).
 the European Bioinformatics Institute. use by non-profit institutions as lo
 Complete proteome
 Transferase; DNA-directed DNA polymerase; DNA replication;
 TIGREAMS; TIGR00594;
 InterPro; IPR003141;
 743
 70
 14 DAMANAYAIEKGKRLEFAGLREMYPGRALPSDANFT----MRMSYGSIKGYEPQDGAWYN
 Local
 IEFEPDLQRTISVDIRYVLFMIDKWGQ 180
 DALENGFEIEK --
 DIFMASSGGGFAYHEAEDYSETEKYDFEKN--LLGIGVTPHPLQNLARRFEGNFTPLA--
 ENQPYKDLADFVEKLPNNFHKKENILPLIQIGAFDYADSNRGKLAYNLADHANLLNYYSD
 YHTTGKGVLEKQDPKSDEFAVQENILDL-----FRTKNYGRYAENGQLHIAFLS--NN
 -QLVKNRRMTILVEINYIRTHRIKIGQ 931
 1 Similarity 45; Conserv
 1060 AA;
 Conservative
 Brassicales;
 Swiss Institute of Bioinformatics
 STANDARD;
 8.6%;
21.7%;
 121571 MW;
 polc;
 PHP_N.
PolC_alpha.
 tRNA_anti
 Brassicaceae; Arabidopsis
 31;
 ---PSINLMKIGDFVKNKKIRLGLAHVQGISRDLAKWIV
 Score 86;
Pred. No. 5
 PRT;
 -FDKNGRLIGLA-----
 Mismatches
 44B03F0937A8D3E6 CRC64;
 321
 moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
 There are no restrictions
 DВ
 Embryophyta; Tracheophyta;
 AA
 1;
 73;
 core eudicots; Rosidae;
 Length 1060;
 Indels
 - FDGNWEAMSGD
 and
 HhoA
 58;
 for
 protease
 Gaps
 commercial
 120
 789
 9
 8
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RA Dose S., de Haan M., Marse A., Schaefer M., Muclier Auer S.,

RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,

RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,

RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,

RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,

RA Neumann S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,

RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,

RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,

RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,

RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,

RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,

RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,

RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,

RA Chefdor F., Cooke R., Berger C., Monfort A., Stocker S.,

Bielke C.,

RA Heijnen L., Haase D., Lemcke K., Mewes H., W., Stocker S.,

Bielke C.,

RA Prishman D., Haase D., Lemcke K., Mewes H., Stocker S.,

Bielke C.,

RA Accaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,

RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,

RA Schnabl S., Shinson D., Sheet P., Cordes M., Abouthrackeh J.,

RA Schnabl T., Kalicki J., Graves T., Harmon G., Edwards J.,

RA Schnabl T., Schutz K., Babott A., Scott K., Johnson D.,

RA Minx P., Bentley D., Mardis E., Dante M., Pepin K., Hillier L.,

RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,

RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,

RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,

RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,

RA Chen E., Marra M., Martienssen R., McCombie W.R.,

RA Chen E., Marra M., Martienssen R., McCombie W.R.,

RA Chen E., Marra M., Martienssen R., McCombie W.R.,
 CHAIN
DOMAIN
ACT_SITE
ACT_SITE
 Hydrolase;
TRANSIT
 Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
Bernelser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
 EMBL; AF114386; AAF24050.1; EMBL; AL021710; CAA16717.1; EMBL; AL161548; CAB78839.1;
 Pfam; PF00089;
 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
 This
 "The chloroplast lumen from Arabidopsis thaliana."; Submitted (JUL-2001) to the SWISS-PROT data bank.
-!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
 Kieselbach T.;
 TRANSIT
 PRINTS; PR00834;
 MEROPS; S01.279;
 SEQUENCE
 Braeken M., V
Weitzenegger
 "Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.":
 InterPro;
 CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A GENE PREDICTION ERROR AND THE FUSION OF THE CDS FOR THIS PROTEIN WITHE CDS FOR A PUTATIVE NUCLEIC ACID BINDING PROTEIN.
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 402:769-777(1999).
 OF 72-82;
 IPR001254; Ser_protease_Try.
 IPR001940; Protease2C
 Serine
 27
72
77
145
186
264
 72-82; 96-110; 150-159; 178-211 AND 306-320. Peterson U., Funk C., Haas B., Schroeder W.
 trypsin; 1.
4; PROTEASES2C
 Bothe
 protease;
 26
71
321
87
145
186
264
 96-110;
 Voet M., Bastiaens I., Aert R.,
 ALT_SEQ.
 Chloroplast; Thylakoid; T
CHLOROPLAST (POTENTIAL).
 POLY-GLU.
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CHARGE RE
 THYLAKOID
 PROTEASE HHOA.
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RESULT 7
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 SQ
 Query Match
Best Local S
Matches 42
 P54627;
01-OCT-1996 (Rel. :
01-OCT-1996 (Rel. :
15-JUN-2002 (Rel. :
 CHAIN
ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
DISULFID
DISULFID
SITE
 Hydrolase;
SIGNAL
 CONFLICT
SEQUENCE
 Drosophila erecta (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7220;
 PRINTS: PR00722; CHYMOTRYPSIN.
SMART; SM00020; TIYP_SPC; 1.
PROSITE: PS50240; TRYPSIN_DOM;
PROSITE: PS00134; TRYPSIN_HIS;
PROSITE: PS00135; TRYPSIN_SER;
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 FlyBase; FBgn0015080; Dere\Try-epsilon
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
 EMBL; U40653; HSSP; P00763;
 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 Wang S., Hickey D.A.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xa
 Trypsin epsilon TRY-EPSILON.
 PROPEP
 Pfam; PF00089;
 MEROPS; S01.112;
 modified
 SEQUENCE
 TRYE_DROER
 286 KGSGMSSGVNF-----AIPIDTVVRTVPYLI 311
 146
 226
 166
 45
 92
 SUBCELLULAR LOCATION: Extracellular.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 ENTLTIGVVSGLGREIPSPNGKSISEAIQTDADINSGNSGGPLLDSYGHTIGVNTATFTR 285
 DAKGTRFSKEGKIVGLDPDNDLAVLKIETEGRELNPVVLGTSNDLRVGQSCFAIGNPYGY 225
 DANFTMRMSYGSIKGYEP-QDGAWYNYHTTGK-----
 NWEAMSGDIEFEPDLQRTISVD - - IRYVLFMI
 ENILDLFRTKNYGRY--AENGQ-LHIAFLSNNDITGGNSGSPVFDKNGRLIGL---AFDG 145
 1 Similarity
42; Conser
 and this statement is not removed.
 40
321 l
 116
210
56
180
206
204
 Conservative
 1DPO.
 AAA83240.1; -.
 AA;
 trypsin;
 STANDARD;
 precursor
protease;
22
30
256
71
116
210
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72
197
230
 34, Created)
34, Last sequence upda
41, Last annotation up
41, Cast annotation up
 40 F
34691 MW;
 8.5%;
 Dere\Try-epsilon
 16;
 BY SIMILARITY.
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CHARGE RELAY SYSTEM
 ACTIVATION PEPTIDE.
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 Pred.
 Score
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 -> G (IN REF. 1) 68DB81E0BD27A7A7
 Mismatches
 85.5;
No. 1
 update)
 Signal; Multigene
 SPECIFICITY
 DB 1;
 -GVLEKQDPKSDEFAV----Q
 Usage
 67;
 Arg-|-Xaa, Lys-|-Xaa
 CRC64;
 Length 321;
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 SIMILARITY)
 SIMILARITY)
SIMILARITY)
(BY SIMILARITY).
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 Matches
 Transferrin-binding protein 2 precursor (TBP-TBPB OR TBP2 OR NMA2025.
 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
 Rajandream M.A., Rutherford K.M., Simmonds M., Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain
 Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davis R.M., Davis R. Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
 STRAIN=22491 / Serogroup A / Serotype 4A;
MEDLINE=20222556; PubMed=10761919;
 Submitted
 complex.
 "Human antibody responses to A and C capsular polysaccharides, protease and transferrin-binding protein complex stimulated by infection with Neisseria meningitidis of subgroup IV-1 or ET-3
 STRAIN=22491 / Serogroup A / Serotype 4A;
Brieske N., Quentin-Millet M.-J., Schenker M.,
 Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
 SEQUENCE
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 TBPB_NEIMA
 NCBI_TaxID=65699
 234
 155
 179
 125
 99
 45
 66
 4 VIAAARAIQADAMANAYAIEKGKRLFFAG------LREMYPGRA-----LPS 44
 anchor (Probable).
 SUBCELLULAR LOCATION: Attached
 VITAAHCLQS-VDAKDLKIRVGSTYWRSGGSVHSVRSFRNHEGYNARTMVNDIAIVRIES 124
 RY
 EΨ
AF058689;
AL162757;
 RTKN----YGRYAENGQLHIAFLSNNDITGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDI 154
 DANFTMRMSYGSIKGYEPQDGA-----WYNYHTTGKGVLEKQDPKSDEFAVQENILDLF 98
 RCRSGEFGYGKKIKDTML-CAYAPNKDACQGDSGGPLV-SGDRLVGVV---SWGYGCGDV
 DLSFRSSIRAVRIADHNPREGATAVVSGWGTTESGGSTIPDHL-----LAVDLEIVDVS 178
 l Similarity
42; Conserv
 156
 235
 (APR-1998) to the
 256
 Conservative
 AA;
 STANDARD;
 AAC13725.1;
CAB85244.1;
 8.4%;
 27612 MW;
 Last sequence update)
 28;
 EMBL/GenBank/DDBJ databases
 Score 84.5;
Pred. No. 1.
 6A9193173D0E37F5 CRC64;
 Mismatches
 to the outer membrane by a lipid
 869
 (TBP-2).
 AA
 DВ
 71; Indels
 1;
 of.
 Skelton J.,
 Schnibbe
 Length 256;
 IS REQUIRED
 Neisseria
 ET-37
 41;
 IgA1
 Gaps
 233
 9
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RESULT 9
 QΥ
 밁
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 В
 Ωy
 Вb
 Ωy
 Дb
 Qy
 DR DR DR FTT FTT SQ
 Matches
 Query Match
Best Local
 Matches
 Query Match
 sequence 504
 Morgan G., Hatfull G., Hendrix R.;
"Genome of bacteriophage Mu and comparison with the Haer
"Influenzae Mu-like prophage FluMu.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: BELONGS TO THE TAIL FIBER FAMILY.
-!- SIMILARITY: SOME, TO H.INFLUENZAE HI1522.
 CHAIN
LIPID
 Outer membrane; Receptor; Signal; Lipoprotein; SIGNAL 1 20 BY SIMILARITY.
 InterPro; IPR000437; Prok_lipoprot.
InterPro; IPR001677; Transferrin_bind.
Pfam; PF01298; Lipoprotein_5; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; FALSE_NEG
 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 S OR 49
 InterPro; IPR005068; Phage_fiber_2.
Pfam; PF03406; Phage_fiber_2; 1.
 EMBL; AF083977; AAF01127.1; -
 the European Bioinformatics Institute. The use by non-profit institutions as long
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
 SEQUENCE FROM N.A.
 Viruses; dsDNA viruses, Mu-like viruses.
 Bacteriophage Mu
 Tail fiber protein (gpS).
 16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
 Q9T1V0;
 SEQUENCE
 NCBI_TaxID=10677;
 VPS_BPMU
 16-OCT-2001
 594
 118
 505
 259
 60
 62
 Local
 Local
 8
 N
YEPODGAWYNYHT - - - - TGKGVLEKODPKSDEFAVO
 PQDGAWYNYHTTGK----GVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFL 117
 SNNDITGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYV 171
 ---GSWYGHIANGTSWSGNASDKEGGNRADFTV-----NFGTKKINGTL-----
 KNSKSAMQAGESSSQADAKTEQVGQSMFLQG--ERTDEKEIPNDQNVVYR----
 KSVIAAARAIQADAMANAYAIEKGKRLFFAGLREMYPGRALPSDANFTMRMSYGSIKGYE 61
 ALSVLVNAIVNGEVISKSAN----GLRIAYGNYGFFIRNDGSNTYFMLTNSGDNMGTYNG
 ARAIQADAMANAYAIEKGKRLFFAGLREMYP--GRALPSDANFTMRM-----SYGSIKG
 46;
 Similarity
37; Conserv
 Similarity
 -TADNRQAATFTIVGDIEGNGFSGT--AKTADSGFDLDQSNNTRTPKAYI 640
 504
 698 AA;
 Conservative
 Conservative
 21
21
 AA;
 STANDARD;
 869
 21
75176 MW;
 55360 MW; C564B6746F53993B CRC64
 8.2%;
19.9%;
 8.3%;
 Last sequence up
 Created)
 no
 RNA stage; Caudovirales; Myoviridae;
 22;
 sequence update)
 24;
 Score 82; DB
Pred. No. 4.8;
 Score 83; D
Pred. No. 5.
 TRANSFERRIN-BINDING PROTEIN 2. N-ACYL DIGLYCERIDE (PROBABLE).
 PRT;
 83FBE14DDF617B1F CRC64;
 Mismatches
 Mismatches
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 There are no restrictions ong as its content is in
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 71;
 71;
 Length 504
 Length 698;
 Complete proteome
 (PROBABLE).
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 Haemophilus
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 92;
 Gaps
 Gaps
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 -!- DOMAIN: CONTAINS A CENTRAL DOMAIN (SUBSTRATE DOMAIN) CONTAINING MULTIPLE POTENTIAL SH2-BINDING SITES AND A C-TERNINAL DOMAIN CONTAINING A DIVERGENT HELIX-LOOP-HELIX (HLH) MOTIF. THE SH2-BINDING SITES PUTATIVELY BIND CRK, NCK AND ABL SH2 DOMAINS. THE HLH MOTIF IS ABSOLUTELY BIND CRK, NCK AND ABL SH2 DOMAINS. THE HLH MOTIF IS ABSOLUTELY REQUIRED FOR THE INDUCTION OF PSEUDOHYPHAL GROWTH IN YEAST AND MEDIATES HETERODIMERIZATION WITH CASL.

-!- DOMAIN: A SERINE-RICH REGION PROMOTES ACTIVATION OF THE SERUM RESPONSE ELEMENT (SRE) (BY SIMILARITY).

-!- DOMAIN: THE SH3 DOMAIN IS NECESSARY FOR THE LOCALIZATION OF THE PROTEIN TO FOCAL ADHESIONS AND INTERACTS WITH ONE PROLINE-RICH REGION OF FOCAL ADHESION KINASE 1.

-!- PTM: FOCAL ADHESION KINASE 1.

-!- PTM: FOCAL ADHESION KINASE 1.

-!- PTM: THE SRC FAMILY KINASES ARE RECRUITED TO THE PHOSPHORYLATED SITES AND CAN PHOSPHORYLATE OTHER TYROSINE RESIDUES. TYROSINE PHOSPHORYLATION IS TRIGGERED BY INTEGRIN
 +
 resistance 1 protein).
BCAR1 OR CRKAS OR CAS.
 30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
CRK-associated substrate (P130CAS) (Breast cancer anti-estrogen
 O61140; Q60869;
30-MAY-2000 (Rel. 39,
30-MAY-2000 (Rel. 39,
15-JUN-2002 (Rel. 41,
 MOUSE
BCA1_MOUSE
 -
 -
 Donaldson J.C., Dempsey P.J., Reddy S., Bouton A.H.,
 MEDLINE=20249316;
 Proc. Natl. Acad.
 MEDLINE=96068679;
 TISSUE-Embryo;
 SEQUENCE FROM N.A. (ISOFORMS CAS-A AND CAS-B), AND INTERACTION WITH
 Mammalia; Eutheria; Rodentia;
 Eukaryota; Metazoa;
 Mus musculus (Mouse).
 kinase substrate pl30Cas."
 FOCAL ADHESION KINASE
 NCBI_TaxID=10090;
 Crk-associated substrate p130(Cas) interacts with nephrocystin and both proteins localize to cell-cell contacts of polarized epithelial
 Polte T.R., Hanks S.K.,
 NTERACTION WITH NEPHROCYSTIN
 432 NYANFDSRYVRDVRLGTQSLTGGLSRDYKAPSGHVITGFHTNGDWEMQGGD 482
 138
 372
 Interaction between
 315
 97
 (BY SIMILARITY). INTERACTS WITH NEPHROCYSTIN AND PTK2B.
SUBCELLULAR LOCATION: FOCAL ADHESIONS. UNPHOSPHORYLATED FORM
LOCALIZES IN THE CYTOPLASM AND CAS TO THE MEMBRANE UPON
TYROSINE PHOSPHORYLATION (BY SIMILARITY).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; CAS-B (SHOWN HERE) AND CAS-A;
ARE PRODUCED BY ALTERNATIVE SPLICING.
 FUNCTION:
 SUBUNIT: FORMS COMPLEXES IN VIVO WITH FOCAL ADHESION KINASE 1,
 Cell Res. 256:168-178(2000).

FUNCTION: DOCKING PROTEIN WHITE PLAYS A CENTRAL COORDINATING ROFORTYROSINE-KINASE-BASED SIGNALING RELATED TO CELL ADHESION.

IMPLICATED IN INDUCTION OF CELL MIGRATION (BY SIMILARITY). HAS
BEEN SHOWN TO BE ESSENTIAL IN CARDIOVASCULAR DEVELOPMENT DURING
 EMBRYOGENESIS
MEDIATED ADHESION OF CELLS TO THE EXTRACELLULAR MATRIX (BY SIMILARITY).
 ADAPTER PROTEIN CRKL AND
 SAQALLRQNHADRKFMIGGLGNKQFGIYMINNSRTANGTDGQAYMDNNGNWLCGAQVIPG
 ----LFRTKNYGRY----AENGQLHIAFLSNNDITGGNSGSPVFDKNGR---
 LRP----LWINNATGAVSMGRGLNVSGDTLSDRFAINSSNGMWIQMRDNNAIFGKNIVNTD
 STANDARD;
 Sci.
 PubMed=10739664;
 PubMed=7479864;
 Chordata;
 focal adhesion kinase
 Created)
 U.S.A. 92:10678-10682(1995).
 LYN KINASE. CAN HETERODIMERIZE WITH
 Craniata; Vert
Sciurognathi;
 PRT;
 874
 ---LIGLAFDGNWEAMSGD 153
 Vertebrata;
 and Crk-associated tyrosine
 Muridae;
 Euteleostomi;
 Coffey R.J.,
 Murinae;
 Mus
 CASL
 ROLE
 431
 137
 371
```

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RESULT 11
BCA1_RAT
 δÃ
 멍
 δÃ
 맑
 Дb
 Ş
 Matches
 Query Match
Sakai R., Iwamatsu A., Hirano N., Ugawa S., Iwama S., Yazaki Y., Hirai H.; Yazaki Y., Hirai H.; "A novel signaling molecule, pl30, forms stable complexes in vivo "A novel signaling molecule, pl30, forms stable complexes in vivo "Crk and v-Src in a tyrosine phosphorylation-dependent manner."; EMBO J. 13:3748-3756(1994).
 BCA1_RAT
Q63767; C
 EMBL; U48853;
EMBL; U28151;
HSSP; P07751;
 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
CRK-associated substrate (P130CAS) (Breast cancer anti-estrogen
 SITE
 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
 This
 MEDLINE=94349922; PubMed=8070403;
 TISSUE=Fibroblast;
 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
 BCAR1 OR CRKAS OR CAS.
 SEQUENCE
 DOMAIN
 PRINTS; PR00452; SH3DOMAIN.
ProDom; PD000066; SH3; 1.
 InterPro; IPR001452; SH3. Pfam; PF00018; SH3; 1.
 or send an email to license@isb-sib.ch).
 between
 SEQUENCE FROM N.A., AND
 resistance 1
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 PROSITE; PS50002; SH3; 1. Phosphorylation; SH3 domain;
 SMART; SM00326; SH3; 1.
 MGD; MGI:108091; Crkas
 entities requires a license agreement (See http://www.isb-sib.ch/announce/
 NCBI_TaxID=10116;
 VARSPLIC
 Alternative
 691
 643
 583
 44
 99
 Local
 4 VIAAARAIQADAMANAYAIEKGKRLFFAGLREMYPG-------RALP 43
 SIMILARITY: CONTAINS 1 SH3 DOMAIN. SIMILARITY: BELONGS TO THE CAS FAMILY.
 NIMRQGK----GQLELQQLKQFERLEQEVSRPIDHDLANWTPAQPLVP--GRTGGL
 SDANFTMRMSYGSIKG-YEPQDGAW---YNY-HTTGKGVLEKQDPKSDEFAVQENILDLF 98
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 SPPKFT--
 LVACSRAVPEDAKQLASFLHGNASLLFRRTKAPGPGPEGSSSLHPNPTDKASSIQSRPLP
 RTKNYGRYAENGQLHTAFLS -------NNDITGGNSGSPVFDKNGRLIGL 141
 43;
 Similarity
 Q63766;
 e splicing.
6 26
74 87
119 420
426 618
639 647
750 800
 874 AA;
 Conservative
 protein).
 1BK2
 AAA93381.1; -.
AAA93248.1; -.
 ·SQDSPDGQYENSEGGWMEDYDYVHLQGKEEFEK-----TQKELLERG
 STANDARD;
 8.2%;
 94256 MW;
 PARTIAL SEQUENCE
 17;
 Score 82;
Pred. No.
 MTVP -> MKYL (IN ISOFORM CAS-A): 5B9EDD76532BDBBA CRC64;
 SH3-binding; Cell adhesion;
 SH3-BINDING (POTENTIAL)
 DIVERGENT HELIX-LOOP-HELIX MOTIF
 SER-RICH
 SUBSTRATE
 PRO-RICH.
 PRT;
 Mismatches
 896
 ø
 FOR KINASES
 DB 1;
 AA
 Usage
 60;
 Length 874;
 Indels
 (BY SIMILARITY).
 ьy
 Murinae; Rattus
 and
 56;
 for
 . 740
 Gaps
 in no way
 with
 642
 9
```

```
Query Match
Best Local 9
 Matches
 the
 adhesion kinase. A putative mechanism for the integrin-mediated tyrosine phosphorylation of Crk-associated substrates."; J. Biol. Chem. 272:29083-29090(1997).
 SEQUENCE
 EMBL; D29766; BAA06169.1;
EMBL; D29766; BAA06170.1;
HSSP; P07751; 1BK2.
 or send an email to license@isb-sib.ch).
 entities requires a license agreement (See http://www.isb-sib.ch/announce/
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 :
 VARSPLIC
 DOMAIN
 Phosphorylation;
 PROSITE; PS50002;
 PRINTS; PR00452; SH3DOMAIN. ProDom; PD000066; SH3; 1.
 Pfam; PF00018; SH3;
 -
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 :
 -
 Hirai H., Morimoto
 Tachibana K., Urano
 MEDLINE=98030588; PubMed=9360983;
 TYROSINE PHOSPHORYLATION BY FOCAL ADHESION KINASE
 DOMAIN
 DOMAIN
 Alternative
 SMART; SM00326;
 InterPro;
 <u>-</u>
 "Tyrosine phosphorylation of Crk-associated substrates by
 DOMAIN
 INTESTINE AND TESTIS.

DOMAIN: CONTAINS A CENTRAL DOMAIN (SUBSTRATE DOMAIN) CONTAINING MULTIPLE POTENTIAL SH2-BINDING SITES AND A C-TERMINAL DOMAIN CONTAINING A DIVERGENT HELLX-LOOP-HELIX (HLH) MOTIF: THE SH2-BINDING SITES PUTATIVELY BIND CRK, NCK AND ABL SH2 DOMAINS: THE HILM MOTIF IS ABSOLUTELY REQUIRED FOR THE INDUCTION OF PSEUDOHYPHAL GROWTH IN YEAST AND MEDIATES HETERODIMERIZATION WITH CASL. DOMAIN: A SERINE-RICH REGION PROMOTES ACTIVATION OF THE SERUM RESPONSE ELEMENT (SRE).

DOMAIN: A DOMAIN IS NECESSARY FOR THE LOCALIZATION OF THE PROCTEIN TO FOCAL ADHESION KINASE 1.
 European Bioinformatics Institute. The by non-profit institutions as long
 SIMILARITY: CONTAINS 1 SH3 DOMAIN. SIMILARITY: BELONGS TO THE CAS FAMILY.
 INTERACTS WITH NEPHROCYSTIN AND PTK2B (BY SIMILARITY)
SUBCELLULAR LOCATION: FOCAL ADHESIONS AND STRESS FIBERS.
UNPHOSPHORYLATED FORM LOCALIZES IN THE CYTOPLASM AND CAN MOVE TO
THE MEMBRANE UPON TYROSINE PHOSPHORYLATION.
THE MEMBRANE UPON TYROSINE PHOSPHORYLATION.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG ISOFORM (SHOWN HERE)
AND A SHORT ISOFORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
AND A SHORT ISOFORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY; WIDELY EXPRESSED. HIGHER EXPRESSION IN LUNG,
 FUNCTION: DOCKING PROTEIN WHICH PLAYS A CENTRAL COORDINATING ROLE FOR TYROSINE KINASE BASED SIGNATION TO CELL ADBESION. IMPLICATED IN INDUCTION OF CELL MIGRATION (BY SIMILARITY).

SUBUNIT: FORMS COMPLEXES IN VIVO WITH FOCAL ADBESION KINASE 1, ADAPTER PROTEIN CRKL AND LYN KINASE. CAN HETERODIMERIZE WITH CASL.
 DISEASE: APPEARS TO HAVE A CENTRAL FUNCTION
 PTM: FOCAL ADHESION KINASE 1 PHOSPHORYLATES THE PROTEIN AT THE YDYVHL MOTIF. THE SRC FAMILY KINASES ARE RECROITED TO THE PHOSPHORYLATED SITES AND CAN PHOSPHORYLATE OTHER TYROSINE RESIDUES. TYROSINE PHOSPHORYLATION IS TRIGGERED BY INTEGRIN MEDIATED ADHESION OF CELLS TO THE EXTRACELLULAR MATRIX.
 1 Similarity
43; Conserv
 CELL TYPES
 IPR001452; SH3.
 splicing.
97 159
168 181
213 514
520 712
733 741
 Conservative
 A,
 SH3; 1.
 SH3 domain;
 SH3;
 T., Fujita H.,
 104262 MW;
 8.18;
%; Score 81; DB
%; Pred. No. 13;
17; Mismatches
 SH3-BINDING (POTENTIAL).
DIVERGENT HELIX-LOOP-HELIX MOTIF
MISSING (IN SHORT ISOFORM).
 SER-RICH
 SUBSTRATE
 PRO-RICH
 SH3-binding; Cell adhesion;
 E861641BFD68D377
 Ohashi Y., Kamiguchi K.,
 DB
13;
 FOR
 There are no restrictions ong as its content is in
 KINASES
 Usage
 Length 968
 IN TRANSFORMATION OF
 CRC64;
 Indels
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 56;
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Gaps
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 RESULT 12
 밁
 MCRB
 Matches
 Query Match
Best Local
 P07955;
01-AUG-1988 (Rel. 0
01-AUG-1991 (Rel. 1
15-JUN-2002 (Rel. 4
 METBA
 InterPro; IPR003179; MCR_beta
Pfam; PF02241; MCR_beta; 1.
Pfam; PF02783; MCR_beta_N; 1.
 This
 from Methanosarcina barkeri.";

Nucleic Acids Res. 15:4350-4551(1987).

-i- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio) ethanesulfonic acid) with 7-mercaptcheptanoylthreonine phosphate to methane and an heterodisulfide.

-i- CATALYTIC ACTIVITY: CH(3)-S-COM + H-S-HTP = CH(4) + COM-S-S-HTP - COFACTOR: THE ENZYME COMPLEX BINDS TIGHTLY (BUT NOT COVALENTLY)

TO TWO MOLECULES OF COENZYME F430. F430 IS A YELLOW NICKEL
 SEQUENCE
 Methanogenesis; Oxidoreductase INIT_MET 0 0
 EMBL; Y00158; CAA68353.1;
 entities requires a license agreement (S or send an email to license@isb-sib.ch).
 use
 STRAIN-Fusaro / DSM 804;
MEDLINE-87231011; PubMed
 Methanosarcina barkeri.
Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
 PIR; A29525; A29525.
HSSP; P11560; 1MRO
 modified and this statement
 the European
 between
 -!- PATHWAY: Methanogenesis; last step.
-!- SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO GAMMA CHAINS.
 Bokranz M., Klein A.;
 SEQUENCE FROM
 MCRB_METBA
 737
 677
 Nucleotide sequence of the methyl coenzyme M reductase
 785
 56
 99
 44
 40
 4
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 PORPHINOID
 NIVRQGK---
--SIKGYEPQDGAWYNYHTTGKGVLEKQDPKS--
 RSVAVNLAGIQG-ALASGKMGGKGRQILGRGLNYDIVGNADAIAENVKKLVQVDEGDDIN
 KSVIAAARAIQADAMANAYAIEKGKRLFFAGLREMYPGR--ALPSDANFTMRMSYG----
 LVACSRAVPEDAKQLASFLHGNASLLFRRTKAPGPGPEGSSSLHLNPTDKASSIQSRPLP 736
 VIAAARAIQADAMANAYAIEKGKRLFFAGLREMYPG-----
 RTKNYGRYAENGQLHIAFLS------NNDITGGNSGSPVFDKNGRLIGL 141
 SPPKFT--
 SDANFTMRMSYGSIKG-YEPQDGAW---YNY-HTTGKGVLEKQDPKSDEFAVQENILDLF 98
 Similarity
 non-profit institutions as long as its content
 433 AA;
 SQDSPDGQYENSEGGWMEDYDYVHLQGKEEFEK-----TQKELLEKG
 STANDARD
 -GQLELQQLKQFERLEQEVSRPIDHDLANWTPAQPLVP--GRTGGL
 08, Created)
19, Last sequence 41, Last annotations
 reductase
 PubMed=3502709;
 45289 MW; BABFA4A3709361A9 CRC64;
 8.0%;
20.1%;
 Last sequence update)
Last annotation updat
 34;
 is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
 beta
 Score 80.5;
Pred. No. 5
 PRT;
 Mismatches
 subunit (EC
 433
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 DВ
 74;
 1;
-----DEFAVQENILDLFR
 .8. -. -).
 Length
 Indels 115;
 -----RALP 43
 gene
 phosphate
 cluster
 Gaps
 98
 99
 55
 784
 13;
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 Вb
 RESULT 13
STSP_STAAU
 20-MAR-1987 (Rel. 04, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glutamyl endopeptidase precursor (EC 3.4.21.19)
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 Staphylococcus aureus. Bacteria; Firmicutes;
 "The
 Staphylococcus
 Carmona C., Gray G.L.;
"Nucleotide sequence of the serine protease gene of Staphylococcus aureus, strain V8.";
Nucleic Acids Res. 15:6757-6757(1987).
 P04188;
InterPro; IPR000126; Ser_proteas_V8.
InterPro; IPR001254; Ser_protease_Try
Pfam; PF00089; trypsin; 1.
 PIR; A26812; PRSASK. MEROPS; S01.269; -.
 EMBL; Y00356; CAA68434.1;
EMBL; AF309515; AAG45843.1
 or send an email to license@isb-sib.ch).
 SEQUENCE FROM N.A. MEDLINE=20569178;
 proteinase)
 STSP_STAAU
 Drapeau G.R.;
 MEDLINE=78212487; PubMed=96922;
 SEQUENCE OF 69-280
 Infect. Immun.
 procease.
 Rice K., Peralta R., Bast D., de Azavedo J., McGavin M.J.; "Description of staphylococcus serine protease (ssp) opero Staphylococcus aureus and nonpolar inactivation of sspA-en
 SEQUENCE
 144
 MEDLINE=87316953;
 167
 204
 122
 100
 264 VIESVVRRAIEAGIISVDKTAPSGYNFYKANDVPKWNAC
 99
 FUNCTION: PREFERENTIALLY CLEAVES PEPTIDE BONDS ON THE CARBOX TERMINAL SIDE OF ASPARTATE AND GLUTAMATE.

CATALYTIC ACTIVITY: Preferential cleavage: Asp-|-Xaa, Glu-|-SIMILARTIY: BELONGS TO PEPTIDASE FAMILY S2B.

DATABASE: NAME-Worthington enzyme manual;

WWW-"http://www.worthington-biochem.com/manual/P/STAP.html".
 primary structure of staphylococcal protease. J. Blochem. 56:534-544(1978).
 AMNASALSSIYEQSGIFEMGGAVGMFERHQLLGLAYQGLNANNLLYDIVKENGKDGTIGT 263
 ITGGNSGSPVFDKNG-------RLIGLAFDG-NWEAMSGDIEFEPDLQRTISV
 TDPYDAPIVKSAVWGSYPQTMDLMGGQVQGILSIPQNNEGLGFSLRNIMANHVAAISNRN
 FROM N.A.
 (V8
 69:159-169(2001).
 STANDARD;
 proteinase) (Endoproteinase Glu-C).
 AAG45843.1; -.
 -LFMID-
 PubMed=3306605;
 -----GKSLL-IQSPKSRIIAGADFMSATTVGAAAVTQTIMDMFG 143
 PubMed=11119502;
 GRYAE----NGQL-----
 Bacillales; Staphylococcus.
 PRT;
 336
 (See http://www.isb-sib.ch/announce/
 KWGQC
 A
 302
 181
 (Staphylococcal serine
 ON THE CARBOXYL-
 sspA-encoded
 operon
 restrictions
 and
 HIAFLSNND
 EMBL
 Glu-|-Xaa
 ST
 a collaboration -
MBL outstation -
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 121
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 no
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POLG_KULT 14

POLG_KUMM
ID POLG_KI
AC P14335
AC P15-JUN
AC F1SULTI
AC COLA G
AC P1-CAM
AC P1-CAM
AC COLA G
AC COLA G
AC P1-CAM
AC COLA G
AC P1-CAM
AC COLA G
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Matches 17
 CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
 ACT_SITE
ACT_SITE
ACT_SITE
 Genome polyprotein [Contains: Capsid protein C (Core protein); Matrix protein (Envelope protein M); Major envelope protein E; Nonstructural proteins NS1, NS2, NS4A and NS4B; Protease/helicase (EC 3.4.21.98) (NS3); RNA-directed RNA polymerase (EC 2.7.7.48) (NS5)]. Kunjin virus (strain MRM61C).
 POLG_KUNJM STANDARD; PRT; 3433 AA. P14335; Q82983; 01-JAN-1990 (Rel. 13, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
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 definitive proteins.";
 MEDLINE-88089524; pubMed=2826659;
Coia G., Parker M.D., Speight G., Byrne M.E., Wes
"Nucleotide and complete amino acid sequences of
definitive gene order and characteristics of the
 CHAIN
 PRINTS; PRO0839; V8PROTEASE. PROSITE; PS00672; V8_HIS; 1. PROSITE; PS00673; V8_SER; 1.
 entities requires a license agreement (S or send an email to license@isb-sib.ch).
 use by non-profit institutions as long modified and this statement is not removed
 J. Gen. Virol. 69:1-21(1988)
 Hydrolase;
SIGNAL
 SEQUENCE FROM N.A.
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae
 SEQUENCE
 PROPEP
 NCBI_TaxID=11078;
 Flavivirus
 233
 123 TGGNSGSPVFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRTISVDIRYVLFMID
 FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B AR HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCT NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION. CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in t
 (RNA)(N).
SUBUNIT: THE VIRION OF THIS VIRUS IS
 precursor polyprotein, commonly with Asp or Glu in the position, Cys or Thr in Pl and Ser or Ala in Pl'. CATALYTIC ACTIVITY: N nucleoside triphosphate = N diph
 PROTEIN M AND GLYCO PROTEIN C AND MRNA.
 LIPOPROTEIN
 TGGNSGSPVFNEKNEVIGIHWGGVPNEFNGAVFINENVRNFLKQNIEDIHFAND
 Similarity
 Serine protease; Zymogen; S1
 Conservative
 30
69
119
161
237
237
1125
145
145
125
229
268
 AA;
 ENVELOPE.
 GLYCOPROTEIN E.
 336
119
161
237
237
125
145
193
229
261
 8.0%;
31.5%;
 36326 MW;
 THE
 13;
 MISSING (IN REF. 3).

MISSING (IN REF. 3).

N -> D (IN REF. 3).

V -> T (IN REF. 3).

D -> N (IN REF. 3).

EFN -> OFD (IN REF. 3).

ENV -> NEVN (IN REF. 3).
 Pred.
 CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
 Score 80;
 GLUTAMYL
 ENVELOPE CONSISTS OF N E. THE NUCLEOCAPSID
 8B138D0C7996AA3E CRC64;
 Mismatches
 No.
 It is produced through
 Signal.
 (See http://www.isb-sib.ch/announce/
 ENDOPEPTIDASE.
 There are no
 DB 1;
 A NUCLEOCAPSID COVERED
 as
 Usage
 24;
 its content
 Westaway E.G.;
of Kunjin virus:
the virus-specified
 Length 336;
 and the
 Indels
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 diphosphate
 NS4B ARE
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EMBL; D00246;

BAA00176.1;

S07

GNWVKV 1SVB.

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 Query Match
Best Local S
Matches 43
 pfam; pr00271; helicase_C; 1.

pfam; pr00869; flavi_glycoprot; 1.

pfam; pr00969; flavi_NS1; 1.

pfam; pr00944; flavi_helicase; 1.

pfam; pr00942; flavi_NS5; 1.

pfam; pr01002; flavi_NS5; 1.

pfam; pr01003; flavi_NS2B; 1.

pfam; pr01004; flavi_NS2B; 1.

pfam; pr01004; flavi_NS2B; 1.

pfam; pr010340; flavi_NS2B; 1.

pfam; pr01340; flavi_NS4B; 1.

pfam; pr01350; flavi_NS4B; 1.

pfam; pr01350; flavi_NS4B; 1.

pfam; pr01570; flavi_NCDPc; 1.

pfam; pr0172B; ftsd; 1.

pfam; pr0172B; ftsd; 1.

pfam; pr0172B; ftsd; 1.

proDom; p0001556; plavi_NS1; 1.

proDom; p0001556; plavi_NS1; 1.

proDom; p0001556; plavi_NS1; 1.

proDom; p0001556; plavi_Sipycoprote; 1.

pn01vrotein. Glycoprote; 1.
 InterPro; IPR001410; DEAD.

InterPro; IPR001059; Flavi_M.

InterPro; IPR001157; Flavi_NS1.

InterPro; IPR000752; Flavi_NS2A.

InterPro; IPR000407; Flavi_NS2B.

InterPro; IPR000404; Flavi_NS4B.

InterPro; IPR001528; Flavi_NS4B.

InterPro; IPR001528; Flavi_NS4B.

InterPro; IPR001038; Flavi_NS5.

InterPro; IPR001380; Flavi_plycoprotE.

InterPro; IPR001850; Flavi_helicase.
 DOMAIN

DOMAIN

NP_BIND

SITE

DISULFID

DISULFID

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DISULFID

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DISULFID

CARBOHYD

CARBOHYD
 CARBOHYD
CARBOHYD
1531
 CHAIN
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 InterPro; IPR002535; Flavi_prope
InterPro; IPR002877; FtsJ.
InterPro; IPR001650; Helicase_C.
 SEQUENCE
 Core protein;
 ATP-binding;
 Polyprotein; Glycoprotein; Transferase; RNA-directed RNA
 52 MSYGSIKGYEPQDGAWYN-----YHTTGKGVLEKQDPKSDEF--AVQENILDLFRTKNY 103
MTRGLLGSYQAGAGVMVEGVFHTLWHTTKGAALMSGEGRLDPYWGSVKEDRL-----CY 1584
 l Similarity
43; Conserv
 1124
216
216
216
216
217
291
792
11375
21256
21256
21506
21506
21509
17990
17990
17990
364
382
382
382
383
3433
 Conservative
 Transmembrane;
 Coat protein;
 AA;
 1143
1374
1505
2124
2273
2528
3433
 8.0%;
 Flavi_propep.
 381363
 28;
 WW;
 Envelope protein; Hydrolase;
Nonstructural protein.
REMOVED FROM CAPSID PROTEIN
 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAN-LINKED) (GLCNAN-LINKED) (GLCNAN-LINKED) (GLCNAN-LINKED) (GLCNAN-LINKED) (GLCNAN-LINKED) (GLCNAN-LINKED) (GLCNAN-LINKED)
 Score 80; DB
Pred. No. 76;
28; Mismatches
 MAJOR ENVELOPE PROTEIN E.
NONSTRUCTURAL PROTEIN NS1.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
PROTEASE/HELICASE (NS3).
 DEAH
 NONSTRUCTURAL PROTEIN NS4A. NONSTRUCTURAL PROTEIN NS4B.
 CAPSID PROTEIN C.
 CELLULAR AMINOPEPTIDASE
 ATP (POTENTIAL).
 INVOLVED IN FUSION.
 RNA-DIRECTED RNA POLYMERASE
 MEMBRANE PROTEIN M
 EE4B888A7D040B99
 BOX.
 80;
 D (GLCNAC...)
D (GLCNAC...)
D (GLCNAC...)
D (GLCNAC...)
 рв
76;
 50;
 Length 3433;
 CRC64;
 Indels
) (POTENTIAL).
) (POTENTIAL).
) (POTENTIAL).
 C
 polymerase;
Helicase;
 (NS5).
 0.8
 γВ
 Gaps
 10;
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RESULT 15
Y030_UREPA
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Search completed: December Job time : 37 secs
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 QΥ
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 Query Match
Best Local
 Matches
 Y030_UREPA
Q9PRB5;
16-OCT-2001
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 STRAIN=Serovar 3;
MEDLINE=20500219; PubMed=11048724;
Glass J.I., Lefkowitz E.J., Glass J.S., Heiner
 NCBI_TaxID=134821;
 Hypothetical UU030.
 SEQUENCE
 Hypothetical protein; TRANSMEM 7 2
 EMBL; AE002102; AAF30435.1; -
 urealyticum.
 Glass J.I.,
Cassell G.H.
 Ureaplasma parvum (Ureaplasma urealyticum biotype 1
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae;
 1705 KTRRIL------PQIIKE 1716
 Nature 407:757-762(2000).
 "The complete sequence of the mucosal pathogen Ureaplasma urealyticum.";
 SEQUENCE FROM N.A.
 16-OCT-2001
16-OCT-2001
 169
 104
 676
 129
 619
 585
 27 RIFFAGLREMYPGRALPSDA---NFTMRMSYGS-IKGYEPQDGAWYNYHTTGKGVLEKQD 82
 VDKNGDVIGLYGNGVIMPNGSYISAIVQGERMDEPVPAGFEPEMLRKKQITVLDLHPGAG 1704
 FDKNGRLIGLAFDG----NWEAMSGDIE----
 GGPWKLQHKWNGQDEVQMIVVEPGKNVKNVQTKPGVFKTPEGEIGAVTLDFPTGTSGSPI 1644
 SMIIDSNFNLVGIHFASLNSRAYGAPNDSMIGNLFVAQSQDLSGDID
 PKSDEFAVQENILDLFRTK---NYGRYAENGQLHIAFLSN------NDITGGNSG 128
 QLFSGG----YPGDVNPNSSAIVSWRGSKSYGSLIQAF-----
 --RYVLFMIDKWGQCPRLIQE
 G----RYAENGQLHIAFL---SNN---
 SPVFDKNGRLIGLAFD----
 Similarity
 DREIKNESILDYYGPKQINNIDGYQKVGEGYLNKLFNVGTRVITSDEIGDLGSGSSG
 747 AA; 85860 MW;
 | (Rel.
| (Rel.
| (Rel.
 (Rel. 40, Create
(Rel. 40, Last s
(Rel. 40, Last a
1 protein UU030.
 Conservative
 STANDARD;
 27
 7.9%;
23.4%;
 Transmembrane; Complete proteome
 Created)
Last sequence update)
Last annotation updat
 20,
 2002,
 187
 21;
 POTENTIAL
 Pred. No.
 Score 79.5;
 68FFD940C28D02AF CRC64;
 PRT;
 -----GNW-----EAMSGDIE
 Mismatches
 747
 13;
 AA
 DB
 FEPDLQRTISVDI-----
 40;
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 C.R., Chen
 Length 747;
 ະ 1).
ae; Ureaplasma.
 155
 722
 -DITGGNSGSPV

 E.Y.,
 67;
 Gaps
 131
 675
 618
 168
 8
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Minimum DB seq length: 0 | Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Total number of hits satisfying chosen parameters:
 Title:
Perfect score:
 OM protein - protein search, using sw model
 Database :
 Searched:
 Scoring table:
 Run on:
 SPTREMBL_21:*
1: sp_archei:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mho:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_roden:*
12: sp_virus:*
13: sp_virus:*
14: sp_unclassifie
15: sp_bacteriap:*
17: sp_archeap:*
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 67.1580 seqs, 206047115 residues
 US-10-008-355-2_COPY_522_712
1003
1 SKSVIAAARAIQADAMANAY.....LEMIDKWGQCPRLIQELKLI 191
 December 20, 2002, 15:04:15; Search time 87 Seconds (without alignments) 452.356 Million cell updates/sec
 GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
sp_plant:*
sp_rodent:*
sp_virus:*
sp_ver(tebrate:*
sp_wer(tebrate:*
sp_rvirus:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
 sp_organelle:*
sp_phage:*
 sp_invertebrate:*
sp_mammal:*
sp_mhc:*
 671580
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| 16     | 15                 | 14     | 13     | 12                 | 11                 | 10     | 9                  | 8      | 7                  | 6                  | U                  | 4                  | · w                | 2                  | . р                |   | Result<br>No.    |
|--------|--------------------|--------|--------|--------------------|--------------------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|---|------------------|
| 89.5   | 89.5               | 89.5   | 89.5   | 89.5               | 89.5               | 89.5   | 89.5               | 89.5   | 89.5               | 89.5               | 90                 | 90.5               | 93                 | 101.5              | 334                |   | Score            |
| 8.9    | . 8.9              | 8.9    | 8.9    | 8.9                | 8.9                | 8.9    | 8                  | 8.9    | 8.9                | 8.9                | 9.0                | 9.0                | 9.3                |                    | ω<br>ω<br>ω        | 1 | Query<br>Match I |
| 3411   | 3411               | 341/1  | 3411   | 3411               | 3411               | 3411   | 3411               | 859    | 856                | 856                | 71/1               | 408                | 513                | 30,5               | 716                |   | Length           |
| 12     | 12                 | 12     | 12     | 12                 | 12                 | 12     | 12                 | 11     | 4                  | 4.                 | N                  | 12                 | 16                 | 16                 | 16                 | : | DB               |
| Q89278 | Q89277             | Q89275 | ONMA60 | C9YWN1             | Q9YWN2             | 091857 | Q98803             | Q8VDM6 | 09вил2             | 076022             | Q51284             | Q96604             | Q97LA8             | Q8XUP6             | Q9PC94             |   | ID               |
|        | Q89277 yellow feve | yellow | yellow | Q9ywn1 yellow feve | Q9ywn2 yellow feve | yellow | Q98803 yellow feve |        | Q9buj2 homo sapien | 076022 homo sapien | Q51284 neisseria m | Q96604 avian infec | Q97la8 clostridium | Q8xup6 ralstonia s | Q9pc94 xylella fas |   | Description      |

| 45                | 44                | 43                 | 42                 | 41     | 40     | 39                 | 38     | 37                 | 36                 | ა<br>5 | 34     | ω<br>ω | 32     | 31                 | 30     | 29     | 28                 | 27                 | 26                 | 25                 | 24     | 23     | 22     | 21                 | 20      | 19                 | 18       | 17                 |
|-------------------|-------------------|--------------------|--------------------|--------|--------|--------------------|--------|--------------------|--------------------|--------|--------|--------|--------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------------------|---------|--------------------|----------|--------------------|
|                   |                   |                    | 81                 |        |        | 81.5               |        | •                  |                    | 82     | 82     | 2.     | 82.5   |                    | 83     | 83     | 83                 | 83                 | 83                 | 83.5               |        |        |        | 85.5               | 86      | σ.                 | 86.5     | 89.5               |
| 8.1               | 8.1               | 8.1                |                    | 8.1    |        | 8.1                |        |                    |                    |        |        |        |        |                    |        |        |                    |                    | 8.3                |                    |        |        |        |                    |         |                    | 8.6      |                    |
| 663               | 663               | 283                | 239                | 239    | 603    | 549                | 493    | 409                | 839                | 798    | 402    | 759    | 726    | 699                | 684    | 682    | 398                | 316                | 263                | 1004               | 729    | 238    | 576    | 323                | 281     | 3411               | 576      | 3411               |
| 16                | 16                | N                  | 16                 | N      | 10     | 10                 | 16     | 12                 | Ç                  | 10     | 16     | 16     | N      | N                  | N      | N      | 11                 | N                  | 16                 | 15                 | 16     | N      | N      | 10                 | 17      | 12                 | N        | 12                 |
| Q8Z597            | Q8ZNL0            | Q9F474             | Q53782             | Q9KH49 | Q9SZT9 | Q93Z39             | Q98PH9 | Q96605             | Q8T6J0             | Q9LLS0 | Q9AB91 | Q92A91 | 030713 | Q9EXC4             | OMdr6Ö | Q9EXB5 | Q8VE75             | Q9FBG1             | Q8RGN9             | Q994B3             | Q8YC77 | Q9FD07 | 085183 | Q93ZW5             | Q8TL57  | Q9YRV3 .           | Q9RF25   | Q89276             |
| Q8z597 salmonella | Q8zn10 salmonella | Q9f474 ehrlichia c | Q53782 staphylococ |        |        | Q93z39 arabidopsis |        | Q96605 avian infec | Q8t6j0 dictyosteli |        |        | -      |        | Q9exc4 neisseria m |        | neis   | Q8ve75 mus musculu | Q9fbgl staphylococ | Q8rgn9 fusobacteri | Q994b3 human immun | ~      |        | C      | Q93zw5 arabidopsis | methano | Q9yrv3 yellow feve | campylob | Q89276 yellow feve |

## ALIGNMENTS

| RAA                                                                     | RA                            | R R<br>A<br>A                                                                                                          | RA                     | RA                                          | RA.                                     | R A              | RA                          | RA                   | ŔA                    | RA                      | RA                  | RA                                          | RA                    | RA               | RA               | RA                                   | RA                                   | RX                   | RC | RΡ                | RN | 0x               | 8 | 8                       | SO                | GN | DE             | DT                 | ŊΊ               | DŢ       | AC      | ID          | RESULT<br>Q9PC94 |
|-------------------------------------------------------------------------|-------------------------------|------------------------------------------------------------------------------------------------------------------------|------------------------|---------------------------------------------|-----------------------------------------|------------------|-----------------------------|----------------------|-----------------------|-------------------------|---------------------|---------------------------------------------|-----------------------|------------------|------------------|--------------------------------------|--------------------------------------|----------------------|----|-------------------|----|------------------|---|-------------------------|-------------------|----|----------------|--------------------|------------------|----------|---------|-------------|------------------|
| de Rosa V.E. :<br>da Silva A.C.I                                        | Peixoto B.R.,                 | Nhani A. Jr.,<br>de Oliveira M.                                                                                        | Moon D.H., Nagai M.A., |                                             |                                         | Machado M A      | Krieger J.E.,               | Ho P.L., Hohei       |                       | Fraga J.S., Fi          | Facincani A.P.      | Coutinho L.L.                               | Colauto N.B.,         | Bueno M.R.P.,    | Barros M.H., I   | Alvarenga R.,                        | Simpson A.J.G.                       | MEDLINE=20365717;    | Þ  | SEQUENCE FROM N.A | Ξ  | NCBI_TaxID=2371; |   | ••                      | Xylella fastidios |    | Hypothetical p |                    | _                | -2000 (  | Q9PC94; | שי          | LT 1<br>.94      |
| V.E. Jr., de Sa R.G., S<br>A.C.R., da Silva A.M.,                       | Peixoto B.R., Pereira G.A.G., | Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,<br>de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Par       | Jai M.A., Nascim       | Miracca                                     |                                         | Madeira A M B N  |                             | Hoheisel J.D., Junqu | •                     |                         | A.P., Ferreira A.J. | Coutinho L.L., Cristofani M., Dias-Neto E., |                       | Camargo A        |                  | Alves L.M.C., Araya J.E., Baia G.S., | Simpson A.J.G., Reinach F.C., Arruda | 717; PubMed=10910347 |    | N.A.              |    | 71;              |   | Proteobacteria; gamma   | liosa.            |    | f1887.         | 21,                | el. 15,          |          |         | RELIMINARY; |                  |
| rigues<br>antelli<br>da Sil                                             | Pereira H.                    | Nunes L.R.,<br>R.C., Palm                                                                                              | Nascimento A.L.T.      | diyaki C.Υ.,                                | E.A.L., Martins E.                      | N Madeira        | Laigret F.,                 | Junqueira M.L.,      | Goldman M.H.S., Gomes | Franco M.C., Frohme M., | S., Ferreir         | Dias-Neto                                   | sta F.F., Co          | Camargo L.E.     | E.D., Bordin S., | \raya J.E.,                          | , Arruda P.,                         | 10347;               |    |                   |    |                  |   | mma subdivision:        |                   |    |                |                    | Last sequenc     | Created) |         | PRT; 716    |                  |
| v., de ROSA A.J.M.,<br>R.V., Sawasaki H.E.,<br>va F.R., Silva W.A. Jr., |                               | Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,<br>de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A., | L.T.O., Netto L.E.S.,  | E.C., Miyaki C.Y., Monteiro-Vitorello C.B., | E.A.L., Martins E.M.F., Matsukuma A.Y., | H M F Marino C I | Lambais M.R., Leite L.C.C., |                      |                       | ohme M., Furlan L.R.,   | C.A., Ferro J.A.,   | Docena C., El-Dorry                         | M.C.R., Costa-Neto C. | Carraro D.M., Ca | Briones          | Baptista C.                          | Abreu F.A., Acencio M.,              |                      |    |                   |    |                  |   | ion; Xanthomonas group; |                   |    |                | annotation update) | sequence update) |          |         | AA.         |                  |

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 QBXUP6 PRELIMINARY; PRT; 305 AA.
QBXUP6; QBXUP6; QCreated)
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative serine protease protein (EC 3.4.21.-)
RSC3140 OR RSQ0463.
 da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A. de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meldanis J., Setubal J.C.; "The genome sequence of the plant pathogen Xylella fastidiosa.", "The 406:151-159(2000).
EMBL; AEOQ4008; AAF84693.1; -.
MEROPS; $46.001; -.
 Siguler P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
EMBL; AL646073; CAD16849.1; -.
 Hydrolase;
SEQUENCE
 InterPro; IPR001254; Ser_protease_Try Pfam; PF00089; trypsin; 1. PRINTS; PR00308; ANTIFREEZEI.
 Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Cholsne N., Claudel-Renard C., Cunnac S., Demang
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex
 MEDLINE=21681879; PubMed=11823852;
 SEQUENCE FROM N.A.
 Bacteria; Proteobacteria;
 Ralstonia solanacearum
 Hypothetical protein; Complete SEQUENCE 716 AA; 79375 MW;
 InterPro; IPR000104; Antifreeze_1
 NCBI_TaxID=305
 710
 186
 650
 126
 591
 546
 43
 16
 8
 æ
 MANAYAIEKGKRLFFAGLREMYPGRALPSDANFTMRMSYGSIK------
 KELNL
 QELKL
ITNCHVLRGGKQVWLK------RGNANFGARLQYPDVERDLCQLRVADFHYPPVT 91
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 ARPIYLQALAD-YNKSHGK-----FVYP-----DANSSLRITFGHVKGYSPKDGVE 590
 NSGSPVLDAHGKLVGLAFDGNWESVSSNWVFDPVMTRTIAVDSRYVQWIMTEVAPAPHLL
 YTPFTTLQGVMAK-NTGVEPFDSPKSLINAIKAKSYANLADQRIGTVPVNFLSDLDITGG
 ARAIQADAMANAYAIEKGKRLFFAGLREMYPGRALPSDANFTMRMSYGSIKGYEPQDGAW 67
 33; Conser
 Similarity
 190
 Complete proteome. 305 AA; 32269 MW;
 Conservative
 Conservative
 33.3%;
 10.18; 24.18;
 (Pseudomonas solanacearum).
ia; beta subdivision; Ralstonia
 40;
 score 101.5;
Pred. No. 0.32
24; Mismatches
 Score 334; DB 16;
Pred. No. 5.1e-22;
0; Mismatches 53;
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 284EC5874BF94327 CRC64;
 .32;
 DB 16;
 53
;
 51;
 CRC64;
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 Indels
 Indels
 de Souza A.A.,
Tsuhako M.H.,
 Length
 , Demange N
Schiex T.,
 group;
 18;
 -GYEPQD 64
 29;
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 Gaps
 Gaps
 649
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RESULT 4
Q96604
ID Q966
AC Q966
DT 01-F
DT 01-F
DT 01-D
DE Nucl
 RESULT
Q97LA8
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 QΥ
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 Query Match
Best Local S
Matches 37
 Pfam; PF00672; HAMP; 1.
Pfam; PF00518; HATPASE_C; 1.
Pfam; PF00512; signal; 1.
PRINTS; PR00344; BCTRLSENSOR.
SMART; SM00387; HATPASE_C; 1.
SMART; SM00388; H1SKA; 1.
 Q96604;
01-FEB-1997
01-FEB-1997
01-DEC-2001
 Q97LA8
Q97LA8;
01-OCT-2001
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Bacteria; Firmicutes; Bacillus
Clostridiales; Clostridiaceae;
 01-OCT-2001 (TYEMBLTel. 18, Created)
01-OCT-2001 (TYEMBLTel. 18, Last sequence up
01-JUN-2002 (TYEMBLTel. 21, Last annotation
Sensory transduction histidine kinase.
 Nucleocapsid
 SEQUENCE
 CAC0654
 InterPro; IPR004359;
 InterPro; IPR003661;
 InterPro;
 InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR004358; Bact_sens_pr_C.
 NCBI_TaxID=1488;
 155
 153
 145
 125
 210
 w
 99
 96
 48
 65
 92
 GNSGSPVFDKNGRLIGL
 NKGFKMTSGEFEAAVMHVLYRRFIYIIFII
 GTKNL-KYYSKGQIFIKDLLKNNMSG--KLSIVTDKNDSVIRIQKIDDSVYDKMFGELSN
 FTMRMSYGSIKGYEPQDGAWYNYHT-----TGKGVLEKQDPKSDEFAVQENILDLF
 RTKNYGRYAENGQLHIAFLSNNDITGGNSGSPVFDKNGRLIGL -- AFDGNWEAMSGDI --
 FVYEKKGGVIDVYKTEKGRYQNKYTQNYLETIFNNGKVIISTILP--DDYS-EDNLSKCY
 GSSGGGLFDANGRLIGI 161
 GAWYNYHTTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITG 124
 LAPGSALVTGQKVYAIGNPLGLELTISEGLISSLRTDDDGRLK----
 Complete proteome.
E 513 AA; 59185 MW; A2F61615182423B3 CRC64;
 Similarity
 FROM
 IPR003660;
 (TrEMBLrel.
 (TrEMBLrel.
 PRELIMINARY;
 Conservative
protein
 I N.A.
 EFEPDLQRTISVDIRYVLFMI 175
 DSM 792 / VKM
 9.3%;
 His_kinA.
HIS_KIN_sig.
 HAMP
 Bacillus/Clostridium group; Clostridia; idiaceae; Clostridium.
 02,
19,
 29;
 Last sequence update)
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 Created)
 Score 93; I
Pred. No. 3.
 Mismatches
 B-1787;
 sequence update)
 408
 513
 DB
3.9;
 AA
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 of the solvent-producing
 16;
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 56;
 Length 513;
 Indels
 -SVQTSAAISR 144
 Zeng Q.,
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 154
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RESULT 5
Q51284
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Matches 37
 Query Match
Best Local S
Matches 38
 O51284

O51284;
O51284;
O51280;
O1-NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
----ferrin-binding protein 2 precursor.
 Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U52600; ABA89161, 1; -
InterPro; IPR001218; Corona_nucleocap.
Pfam; PF00937; Corona_nucleoca; 1.
SEQUENCE 408 AA; 4547c.
 Signal.
SIGNAL
CHAIN
 MEDLINE=97124667; PubMed=8955062; Sapats S.I., 'Ashton F., Wright P. "Novel variation in the N protein
 SEQUENCE
 InterPro; IPRO(
Pfam; PF01298;
 Legrain M., Findeli A., Villeval D., Quentin-Negrain M., Findeli A., Villeval D., Quentin-Nedecular characterization of hybrid transfer from Neisseria meningitidis.";
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ EMBL; Z50731; CAA90598.1;
 Neisseria meningitidis.
Bacteria; Proteobacteria;
 Virology 226:412-417(1996).
 virus."
 SEQUENCE FROM N.A.
 NCBI_TaxID=11120;
 Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
 Avian infectious bronchitis virus.
 STRAIN-BZ163;
 SEQUENCE FROM N.A.
 NCBI_TaxID=487;
518
 150
 113
 92
 67
 32
 25
 Local Similarity
 N
 GQASWFQSLKEKKRTGEPPTFEGSGVPDNSNVKPQFQHGYWKRQRRYKSGKGGRKPVADA
 HIAFLSNN-----DITGGNSGS
 GKRLFFAGLRE-----MYPGRALPSDANFTMRMSYGSIK------GYEPQDGA 66
KNSKSAMQAGESSSQADAKTEQVGQSMFLQG--ERTDEKEIPSEQNIVYR----
 KSVIAAARAIQADAMANAYAIEKGKRLFFAGLREMYPGRALPSDANFTMRMSYGSIKGYE
 WYFYYTGTGPFGDLEWGDPNDDVVWVKAKGADTSKIGNYGVRDPDKFDQAPLRFIEGG-- 149
 WYNYHT-TGK-GVLEKQDPKSDEFAVQENILDLFRTKNYG-----
 38;
 Similarity
 IPR001677; Transferrin_bind 1298; Lipoprotein_5; 1.
 1
21
711 AA;
 PNNFRWDFIALSRGRNGS
 Conservative
 Conservative
 20 P
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77057 MW;
 F., Wright P.J.,
the N protein of
 9.0%;
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 . 88;
 beta
 17;
 28;
 Score 90.5; DI
Pred. No. 4.9;
17; Mismatches
 Score 90; DB
Pred. No. 12;
28; Mismatches
 POTENTIAL.
TRANSFERRIN-BINDING PROTEIN
; 9BC8A1671F6991D0 CRC64;
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 Quentin-Millet M.,
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RESULT 7
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 Q9BUJ2; Q9UG75; 09UG75; 01-JUN-2001 (TIEMBLIEL 17, C: 01-JUN-2001 (TIEMBLIEL 17, L: 01-JUN-2002 (TIEMBLIEL 21, L: ELB-55kDa-associated protein
 076022 PRELIMINARY;
076022;
01-NOV-1998 (TrEMBLrel, 0)
01-NOV-1998 (TrEMBLrel, 0)
01-JUN-2002 (TrEMBLrel, 2)
 "EIB-55kilodalton-associated protein: binding activity implicated in nucleoc adenovirus and cellular mRNAs.";
J. Virol. 72:7960-7971(1998).
EMBL; AJ0075599; CAA07548.1;
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SMART; SM00449; SPRY; 1.
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SEQUENCE FROM N.A.
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 337
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 306
 249 SYGVRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQLGEEPFS---YGYG 305
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 607
 118
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 72
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42; Conserv
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IPR003877; SPRY_receptc
 Schuett H.,
 Conservative
 Chordata;
Primates;
 8.9%;
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01-MAR-2002
 SEQUENCE FROM N.A.
Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases EMBL; BC021506; AAH21506.1; -.
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 250
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 19 AYAIEKGKRLFFAGLREMYPGRALPSDA--NFTMRM-----SYGSIKGYEPQDGAWYNYH 71
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 (FEB-2001) to the EMBL/GenBank/DDBJ databases
 al protein.
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 Heubner D., Mewes H.W.,
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 SEQUENCE FROM N.G.,

STRAIN-85-82H IVORY COAST;

Pisano M.R., Tolou H., Nicoli J.;

"Homogeneity of Yellow fever virus strains isolated during
 PROSITE; PS009bz; NIBOULLE | PS009bz; NIBOULLE
 Pfam;
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Pfam;
 01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
1542
 and post epidemic period in west Africa."; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases EMBL, U54798; AAA99812.1; -. HSSP; P14336; 1SVB.
 Pfam; PF00271; helicase_C; 1.
ProDom; PD001496; Flavi_NS1; 1.
ProDom; PD001556; Flavi_glycoprotE; 1.
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 Pfam;
 Pfam;
 Pfam;
 Pfam;
 Flavivirus.
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Yellow fever virus
 Polyprotein.
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PF02832; Flavi_he__

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PF00972; Flavi_NS5; 1.
PF01570; Flavi_propep; 1.
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39; Conser
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 IPR000487;
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 IPR000336; Flavi_glycoprotE.
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 IPR000752;
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 PRO01865; Ribosomal_S2.
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 Flavi_NS5
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 Helicase_C
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 21;
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SEQUENCE 3411 AA; 379584
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 MEDLINE=98376360; PubMed=9712515; Xie H., Cass A.R., Barrett A.D.T.; "Yellow fever 17D vaccine virus isolated accumulates very few mutations."; Virus Res. 55:93-99(1998).
 STRAIN=17D-204-USA VACCINE
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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IPR000752; I
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IPR000336; Flavi_glycoprotE.
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 Flavi_NS4A.
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Score 89.5; DB 12; Pred. No. 1.1e+02; l; Mismatches 46;
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Viruses; ssRNA positive-strand viruses,
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 01-MAY-1999
01-MAY-1999
 1626 IVNRNGEVIGLYGNG---ILVGDNSFVSAISQT 1655
 1542
 EMBL; AF052444; AAC35906.1;
 fever 17D vaccine virus.";
J. Gen. Virol. 79:1895-1899(1998).
 Xie H., Ryman K.D., Campt
"Mutation in NS5 protein
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 01-MAR-2002
 Q9YWN2;
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 InterPro;
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Flavi_NS2B.
Flavi_NS4A.
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Flavi_NS5.
 Flavi_NS1.
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 Flavi_capsidC.
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 -----IPSWASVKEDLVAYG---GSWKLEGRWDGEEEVQLIA 1585
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 Created)
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 8AAC0F24F65DC50C CRC64;
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 3411
 mouse neurovirulence
 163
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 DNA stage;
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 InterPro; IPRO01865; Ribosomal_S2.

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Pfam; PF00869; Flavi_glycoprot; 1.

Pfam; PF00849; Flavi_helicase; 1.

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 "Mutation in NS5 protein attenuates mouse neurovirulence fever 17D vaccine virus.";
J. Gen. Virol. 79:1895-1899(1998).
 STRAIN-17D-204-SOUTH AFRICA VACCINE;
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Xie H., Ryman K.D., Campbell G.A., Barrett
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 Flavi_propep;
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Flavi_NS2B.
Flavi_NS4B.
Flavi_NS4B.
Flavi_NS5.
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 Query Match
Best Local :
 Matches
 Q89275
Q89275;
Q1-NOV-1996
Q1-DEC-2001
Q1-JUN-2002
 InterPro;
InterPro;
 Pfam;
Pfam;
Pfam;
Pfam;
 Pfam;
Pfam;
 InterPro;
InterPro;
 ProDom; PD001496; Flavi_NS1; 1.
ProDom; PD001556; Flavi_glycoprotE; 1.
SMART; SM00490; HELICC; 1.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
 EMBL; U17066; AAC54267.1; -
 Submitted
 STRAIN-VACCINE
 STRAIN=VACCINE STRAIN 17DD;
MEDLINE=95274286; PubMed=7754673;
 Viruses; ssRNA positivė-strand viruses, no DNA stage; Flaviviridae;
 Yellow fever virus.
 1626
 1542
 ATP-binding; Helicase. SEQUENCE 3411 AA; 3
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 InterPro;
 InterPro;
 InterPro;
 InterPro;
 InterPro;
 HSSP; P14336;
 Galler R.;
 SEQUENCE FROM N.A.
 NCBI_TaxID=11089;
 InterPro;
 InterPro;
 InterPro;
 [nterPro;
 L7DD
 Complete nucleotide sequence
 131
 14
 19
 72
rrro; IPR001650; Helicase_C.
rrro; IPR001665; Ribosomal_S2.
r; PF01003; Flavi_cdpsid; 2.
r; PF00869; Flavi_glycoprot; 2.
r; PF02832; Flavi_glycop_C; 2.
r; PF02832; Flavi_helicase; 2.
r; PF01004; Flavi_M; 2.
r; PF01004; Flavi_NS1; 2.
 Santos C.N., Post P.R., Carvalho R., Ferreira I.I.,
 and 17D-213
 IVNRNGEVIGLYGNG---ILVGDNSFVSAISQT 1655
 AVPGKNVVNVQTKPS-
 AFLVRNGKKL------IPSWASVKEDLVAYG---GSWKLEGRWDGEEEVQLIA 1585
 AYAIEKGKRLFFAGLREMYPGRALPSDANFTMRM-SYGSIKGYEPQDGAWYNYH-----
 VFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRT 163
 -TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSP 130
 Similarity
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IPR000752; Flavi_NS2A.
; IPR000487; Flavi_NS2B.
; IPR000404; Flavi_NS4B.
; IPR001528; Flavi_NS4B.
 FROM N.A.
 IPR001122; Flavi_capsidC.
IPR000336; Flavi_glycoprotE.
IPR001850; Flavi_helicase.
IPR000069; Flavi_M.
 IPR000208; Flavi_NS5.
IPR002535; Flavi_propep.
 (NOV-1994) to the EMBL/GenBank/DDBJ databases
 IPR002877; FtsJ.
 35:35-41(1995).
 (TrEMBLrel, 01, (TrEMBLrel, 19, (TrEMBLrel, 21,
 Conservative
 PRELIMINARY;
 1SVB
 STRAIN 17DD;
 25.5%;
 379500 MW;
 21;
 Last sequence up
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Pred. No. 1.1e+02;
1; Mismatches 46;
 of yellow
 PRT;
 -LFKVRNGG---EIGAVAL-----DYPSGTSGSP 1625
 8A9B127F6623A933
 fever virus
 A
 update)
 update)
 Length
 CRC64;
 Indels
 vaccine strains
 Rice C.M.,
 47;
 Gaps
 71
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RESULT 15
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 Query Match
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Matches 39
 Pfam; PF01005; Flavi_NS2A; 2.
Pfam; PF01302; Flavi_NS4B; 2.
Pfam; PF01350; Flavi_NS4B; 2.
Pfam; PF01349; Flavi_NS4B; 2.
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Pfam; PF01072; Flavi_propep; 2.
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Pfam; PF00271; helicase_C; 2.
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ProDom; PD001556; Flavi_glycoprotE; 1.
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CHAIN 211 285
CHAIN 211 285
CHAIN 216 778
CHAIN 779 1187
CHAIN 1188 1354
CHAIN 1355 1483
CHAIN 1355 1483
CHAIN 2108
CHAIN 2108 2394
CHAIN 2507 2507
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Q89277;
Q1-NOV-1996
Q1-DEC-2001
 CHAIN
SEQUENCE
 strain of yellow fever virus with neurotropic vaccine.";
J. Gen. Virol. 76:2749-2755(1995)
 SEQUENCE FROM N.A.
STRAIN-FRENCH NEUROTROPIC VIRUS;
MEDLINE-96068808; PubMed-7595382;
Wang E., Ryman K.D., Jennings A.D.,
Sanders P.G., Barrett A.D.;
"Comparison of the genomes of the way
 SMART;
 Submitted (FEB-1995) to the EMBL/GenBank/DDBJ EMBL; U21055; AAA99712.1; -. HSSP; P14336; ISVB.
 Wang
 1586
 SEQUENCE FROM
STRAIN-FRENCH
 Flavivirus
 Viruses; ssRNA positive-strand
 01-JUN-2002
 1626 IVNRNGEVIGLYGNG---ILVGDNSFVSAISQT 1655
 1542 AFLVRNGKKL-
 SMART:
 NCBI_TaxID=11089;
 Yellow fever virus
 PROSITE;
 131
 72
 19
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E3
 VFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRT
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 AYAIEKGKRLFFAGLREMYPGRALPSDANFTMRM-SYGSIKGYEPQDGAWYNYH------
 -TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSP 130
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SM00490; HELICC; 2.
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 39; Conservative
IPR001410; DEAD
 211
286
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 (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
 PRELIMINARY;
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 NEUROTROPIC VIRUS;
 AA;
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 - IPSWASVKEDLVAYG
 MW;
 Last sequence update)
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 Created)
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NS3.
POTENTIAL.
 Score 89.5; DB 1:
Pred. No. 1.1e+02
l; Mismatches 4
 NS5.
 NS1.
 ENVELOPE PROTEIN.
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 viruses,
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 3411
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 163
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 12;
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 GSWKLEGRWDGEEEVQLIA 1585
 Taffs F.,
 Length
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 Indels
 Flaviviridae;
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Search completed: December 20, Job time: 104 secs
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 Query Match
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Matches 39
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 SEQUENCE
 ATP-binding;
 72 -TTGKGVLEKQDPKSDEFAVQENILDLFRTKNYGRYAENGQLHIAFLSNNDITGGNSGSP 130
 19 AYAIEKGKRLFFAGLREMYPGRALPSDANFTMRM-SYGSIKGYEPQDGAWYNYH-----
 / Match 8.9%; Score 89.5; DB 12; Length 3411; Local Similarity 25.5%; Pred. No. 1.1e+02; nes 39; Conservative 21; Mismatches 46; Indels 47;
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IVNRNGEVIGLYGNG---ILVGDNSFVSAISQT 1655
 VFDKNGRLIGLAFDGNWEAMSGDIEFEPDLQRT 163
 AFLVRNGKKL-----IPSWASVKEDLVAYG---GSWKLEGRWDGEEEVQLIA 1585
 PS00962; RIBOSOMAL_S2_1; UNKNOWN_2.
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3411 AA;
 Helicase. 121
2 112
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179 1187
179 1187
1484 1354
1484 2106
2108 2394
2395 2506
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 2002, 17:30:35
 NS1.
NS2A.
NS2B.
NS3.
NS4A.
NS4B.
NS5.
 M PROTEIN.
 ENVELOPE PROTEIN E.
 Indels 47;
 Gaps
 71
 8
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